

# SEARCH REQUEST FORM

Scientific and Technical Information Center

Requestor's Name: David Lukton Examiner number: 71263 Date: 5/24/04

Art Unit: 1653 Phone number: 571-272-0952 Serial Number:

09-765105

Mail Box: 3-C-70 Examiner Rm: 3-B-75 Results format: paper

\*\*\*\*\*

Title of Invention: C-TERMINAL MODIFIED OXAMYL  
DIPEPTIDES AS INHIBITORS OF THE ICE-CED-3 FAMILY OF  
CYSTEINE PROTEASES

Applicants: KARANEWSKY, DONALD S., TERNANSKY, ROBERT  
J., LINTON, STEVEN D., DINH, THANG

Earliest Priority Date: 7/2/98

\* \* \* \*

Please search the sequences in this case

182 AA's

## STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: _____	NA Sequence (#) _____	STN _____
Searcher Phone #: _____	AA Sequence (#) <u>2</u>	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searched Picked Up: <u>5/24/04</u>	Bibliographic _____	Dr. Link _____
Date Completed: <u>5/25/04</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems <u>QSP</u>
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Fee: _____	Other _____	Other (specify) _____

Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions **.rnpm** and **.rnpn**

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions **.rapm** and **.rapn**

***Because they contain data that is confidential, the results of Pending database searches should not be left in the case .***



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 122770**

**TO: David Lukton**  
**Location: rem/3b75/3c70**  
**Art Unit: 1653**  
**Tuesday, May 25, 2004**

**Case Serial Number: 09/765105**

**From: Edward Hart**  
**Location: Biotech-Chem Library**  
**REM-1A55**  
**Phone: 571-272-2512**

**edward.hart@uspto.gov**

### **Search Notes**

Examiner Lukton,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



# STIC SEARCH RESULTS FEEDBACK FORM

## Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or *contact:*

Mary Hale, Information Branch Supervisor  
571-272-2507 Remsen E01 D86

## Voluntary Results Feedback Form

➤ I am an examiner in Workgroup:  Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature  
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library Remsen Bldg.



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 24, 2004, 14:36:17 / Search time 51 Seconds  
(without alignments)  
22.161 Million cell updates/sec

Title: US-09-765-105A-1

Perfect score: 21

Sequence: 1 YVAD 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Jan04.\*

- 1: Genesep1980s.\*
- 2: Genesep1990s.\*
- 3: Genesep2000s.\*
- 4: Genesep2001s.\*
- 5: Genesep2002s.\*
- 6: Genesep2003as.\*
- 7: Genesep2003bs.\*
- 8: Genesep2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	21	100.0	4	2	AAR34789 Interleuk
2	21	100.0	4	2	AAR34621 Chromoph
3	21	100.0	4	2	AAR32544 Chromoph
4	21	100.0	4	2	AAR34822 Chromoph
5	21	100.0	4	2	AAR51047 Sequence
6	21	100.0	4	2	AAR77200 Cell prol
7	21	100.0	4	2	AAR95702 Tetrapept
8	21	100.0	4	2	AAR98753 Asp-ase i
9	21	100.0	4	2	AAW00214 Ich-2 sub
10	21	100.0	4	2	AAW06453 ICE pepti
11	21	100.0	4	2	AAW45979 Cysteine
12	21	100.0	4	2	AAW76199 Mouse cas
13	21	100.0	4	2	AAW52749 Aminometh
14	21	100.0	4	2	ABP71236 ICE-speci
15	21	100.0	4	2	AAW56304 Peptide c
16	21	100.0	4	2	AAW65067 ICE bindi
17	21	100.0	4	2	AAV15619 Peptide u
18	21	100.0	4	2	AAV30071 N-substit
19	21	100.0	4	2	AAV04112 Enzyme co
20	21	100.0	4	2	AAW68555 Interleuk
21	21	100.0	4	2	AAV24410 Caspase p
22	21	100.0	4	2	AAW99674 ICE prote
23	21	100.0	4	2	AAW94092 Protease
24	21	100.0	4	2	AAW94094 Protease
25	21	100.0	4	3	AAV69647 Caspase i

26	21	100.0	4	3	AAV99959	Aay99959 Tetrapept
27	21	100.0	4	3	AAV49941	Aay49941 Synthetic
28	21	100.0	4	3	AAB26850	Aab26850 Synthetic
29	21	100.0	4	3	AAV80783	Aay80783 Fluoropho
30	21	100.0	4	3	AAV69867	Aay69867 ICE cleav
31	21	100.0	4	3	AAV67492	Aay67492 Caspase 1
32	21	100.0	4	3	AAV67492	Aay67492 APP agon1
33	21	100.0	4	3	AAV81938	Aay81938 Caspase s
34	21	100.0	4	3	AAV87640	Aay87640 Caspase s
35	21	100.0	4	3	AAB26703	Aab26703 Caspase s
36	21	100.0	4	3	AAB03094	Aab03094 Substrate
37	21	100.0	4	3	AAV56899	Aay56899 Caspase i
38	21	100.0	4	3	AAV57442	Aay57442 Peptide A
39	21	100.0	4	3	AAB28539	Aab28539 Caspase-1
40	21	100.0	4	3	AAB32119	Aab32119 Tetrapept
41	21	100.0	4	4	AAB59584	Aab59584 Caspase-1
42	21	100.0	4	4	AAV62548	Aag62548 Cresyl vi
43	21	100.0	4	4	AAV67379	Aag67379 Peptide s
44	21	100.0	4	4	AAV72472	Aay72472 YVAD pept
45	21	100.0	4	4	AAV64408	Aag64408 Caspase p
				4	AAB91890	Aab91890 Apoptosis

ALIGNMENTS

RESULT 1  
AAR34789  
ID AAR34789 standard; peptide; 4 AA.  
XX

AC AAR34789;  
XX

XX 25-MAR-2003 (revised)  
DT 08-JUL-1993 (first entry)

XX  
DE Interleukin-1beta convertase activity determining peptide.

XX ICE; interleukin-1beta convertase; activity; chromophore contg;  
KW monitoring; IL-1 mediated diseases; ICE inhibitor evaluation; diagnosis.

XX Synthetic.

XX Key Location/Qualifiers  
FH Modified-site 1

FT /note= "N-acetyl-Tyr"  
FT Modified-site 4

FT /note= "Asp-p-nitroanilide, Asp-6-aminoquinoline amide or  
FT /note= "Asp-7-amino-4-methylcoumarin amide"

XX EF533226-A2.  
XX 24-MAR-1993.

XX 08-AUG-1992; 92EP-00202449.  
XX 16-AUG-1991; 91US-00746524.

XX 17-DEC-1991; 91US-00808996.  
XX (MERI ) MERCK & CO INC.

XX Chapman KT, Maccross M, Mumford RA, Thornberry NA, Weidner JR;  
XX WPI; 1993-095531/12.

XX New chromophore-contg. peptide derivs. - for determining interleukin-1-  
XX beta convertase activity in the diagnosis of inflammatory and immune-  
XX based conditions.

XX Example; Page 26; 41pp; English.

XX The peptide is a chromophore contg. compound which is useful in  
XX determining interleukin-1beta convertase (ICE) activity and is therefore  
XX useful in diagnosis and monitoring of IL-1 mediated diseases or in  
XX evaluation of ICE inhibitors. IL-1 has been implicated in meningitis,

CC salpingitis, complications of septic shock, disseminated intravascular  
CC coagulation; adult respiratory distress syndrome, inflammation due to  
CC antigen, antibody and/or complement deposition, arthritis, cholangitis,  
CC colitis, encephalitis, endocarditis, glomerulonephritis, hepatitis,  
CC myocarditis, pancreatitis, pericarditis, reperfusion injury, and  
CC - rejection, graft-v-host disease, and autoimmune diseases including Type I  
CC diabetes mellitus and multiple sclerosis. IL-1 has also been implicated  
CC in treatment of bone and cartilage resorption, or diseases causing  
CC excessive extracellular matrix deposition. These include periodontal  
CC disease, interstitial pulmonary fibrosis, cirrhosis, systemic sclerosis,  
CC or keloid formation. To use the peptide in an assay, the peptide, ICE, or  
CC cleaves the chromophore bond, and the ICE activity is then determined by  
CC spectrophotometric or fluorimetric analysis. Leucine amino- peptidase  
CC microsomal (LAPM) is the most pref. enzyme in the disclosure. The peptide  
CC is used in concns. of 1 uM to 10 mM. (Updated on 25-MAR-2003 to correct  
CC PN field.)  
XX  
SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
|  
|  
|  
|  
Db 1 YVAD 4

RESULT 2  
ID AAR34621 standard; peptide; 4 AA.  
XX AAR34621;  
XX  
XX 25-MAR-2003 (revised)  
DT 12-NOV-1992 (first entry)  
XX  
XX Chromophore-contg. cpd. for determining ICE activity (1).  
XX Interleukin-lbета; IL-lb; inflammation; immune; disease; diagnosis;  
KW p-nitroanilide.  
XX  
XX Synthetic.

Key Location/Qualifiers  
FT Modified-site 1 /note= "N-acetyl-tyrosinyl"  
FT Modified-site 4 /note= "aspartic acid p-nitroanilide"

EP528487-A2.  
XX  
XX 24-FEB-1993.  
XX  
XX 08-AUG-1992; 92EP-00202450.  
XX  
XX 16-AUG-1991; 91US-00746455.  
PR 17-DEC-1991; 91US-00808994.  
XX  
XX (MERI ) MERCK & CO INC.

Chapman KT, Thornberry NA, Maccoss M, Weidner JR, Mumford RA;  
PI Hagmann WK;  
XX  
XX WPI; 1993-060350/08.  
XX  
XX New chromophore-contg. cpds. - for determining interleukin-lbета  
PT convertase activity in diagnosis of inflammatory or immune-based  
PT disorders.  
XX  
XX Claim 9; Page 42; 42pp; English.

XX The cpd. is used for determining interleukin-lbета convertase (ICE)  
CC activity. ICE has been implicated in inflammatory and immune-based  
CC diseases including diseases of the lungs and airways, CNS, eyes, ears,  
CC joints, bones and connective tissues, cardiovascular system (including  
CC the pericardium), GI and urogenital systems and skin and mucosal  
CC membranes. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
|  
|  
|  
|  
Db 1 YVAD 4

RESULT 3  
ID AAR32544 standard; peptide; 4 AA.  
XX AAR32544;  
XX  
XX 25-MAR-2003 (revised)  
DT 12-NOV-1992 (first entry)  
XX  
XX Chromophore-contg. cpd. for determining ICE activity (5).  
XX Interleukin-lbета; IL-lb; inflammation; immune; disease; diagnosis;  
KW 7-amino-4-methylcoumarin.  
XX  
XX Synthetic.

Key Location/Qualifiers  
FT Modified-site 1 /note= "N-acetyl-tyrosinyl"  
FT Modified-site 4 /note= "aspartic acid 7-amino-4-methylcoumarin"

EP528487-A2.  
XX  
XX 24-FEB-1993.  
XX  
XX 08-AUG-1992; 92EP-00202450.  
XX  
XX 16-AUG-1991; 91US-00746455.  
PR 17-DEC-1991; 91US-00808994.  
XX  
XX (MERI ) MERCK & CO INC.  
XX  
XX Chapman KT, Thornberry NA, Maccoss M, Weidner JR, Mumford RA;  
PI Hagmann WK;  
XX  
XX WPI; 1993-060350/08.

New chromophore-contg. cpds. - for determining interleukin-lbета  
PT convertase activity in diagnosis of inflammatory or immune-based  
PT disorders.  
XX  
XX Example 8; Page 31; 42pp; English.  
XX  
XX The cpd. is used for determining interleukin-lbета convertase (ICE)  
CC activity. ICE has been implicated in inflammatory and immune-based  
CC diseases including diseases of the lungs and airways, CNS, eyes, ears,  
CC joints, bones and connective tissues, cardiovascular system (including  
CC the pericardium), GI and urogenital systems and skin and mucosal  
CC membranes. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
XX Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
DB 1 YVAD 4

RESULT 4  
AAR34622 standard; peptide; 4 AA.  
ID AAR34622  
XX AC AAR34622;  
XX AC AAR34622;  
XX AC AAR34622;  
DT 25-MAR-2003 (revised)  
DT 12-NOV-1992 (first entry)  
XX DE Chromophore-contg. cpd. for determining ICE activity (2).  
XX DE Interleukin-1b; IL-1b; inflammation; immune; disease; diagnosis;  
KW 6-aminoquinoline amide.  
XX OS Synthetic.  
XX OS Synthetic.  
FH Key Location/Qualifiers  
FT Modified-site 1  
FT Modified-site 4 /note= "N-acetyl-tyrosinyl"  
FT Modified-site 4 /note= "aspartic acid 6-aminoquinoline amide"  
XX EP528487-A2.  
XX 24-FEB-1993.  
XX 08-AUG-1992; 92EP-00202450.  
XX 16-AUG-1991; 91US-00746455.  
XX 17-DEC-1991; 91US-00808994.  
XX (MERI ) MERCK & CO INC.  
XX Chapman KT, Thornberry NA, Maccoss M, Weidner JR, Mumford RA;  
PI Hagmann WK;  
XX WPI; 1993-060350/08.  
XX New chromophore-contg. cpds. - for determining interleukin-1b  
FT convertase activity in diagnosis of inflammatory or immune-based  
PT disorders.  
XX Claim 9; Page 42; 42pp; English.  
XX The cpd. is used for determining interleukin-1b convertase (ICE)  
CC activity. ICE has been implicated in inflammatory and immune-based  
CC diseases including diseases of the lungs and airways, CNS, eyes, ears,  
CC joints, bones and connective tissues, cardiovascular system (including  
CC the pericardium), GI and urogenital systems and skin and mucosal  
CC membranes. (Updated on 25-MAR-2003 to correct PN field.)  
XX SQ Sequence 4 AA;  
Query Match 100.0%; Score 21; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
DB 1 YVAD 4

RESULT 5  
AAR51047 standard; protein; 4 AA.  
ID AAR51047

XX AAR51047;  
XX 25-MAR-2003 (revised)  
DT 07-OCT-1994 (first entry)  
XX DE Sequence of tetrapeptide aldehyde inhibitor of murine precursor  
DE interleukin-1 beta (pre-IL-1 beta) converting enzyme (ICE).  
XX KW Interleukin-1 beta converting enzyme; mature interleukin; inhibitor; ss.  
XX OS Synthetic.  
XX Key Location/Qualifiers  
FH Modified-site 1  
FT Modified-site 4 /label= Ac  
FT Modified-site 4 /label= CHO  
XX WO9406906-A1.  
XX 31-MAR-1994.  
XX 09-SEP-1993; 93WO-US008479.  
XX 18-SEP-1992; 92US-00947330.  
XX (MERI ) MERCK & CO INC.  
XX Molineaux SM, Rolando AM, Casano FJ;  
XX WPI; 1994-118456/14.  
XX DNA encoding murine precursor interleukin 1 beta converting enzyme - for  
FT producing ICE and its subunits and for identification of inhibitors of  
FT ICE activity.  
XX Disclosure; Page 15; 87pp; English.  
XX cDNA encoding murine pre-IL-1 beta converting enzyme (ICE) was isolated  
CC from IL-1 producing mouse cells. Murine ICE cleaves the peptide bond  
CC between Asp17 and Val118 of murine precursor IL-1 beta, and the peptide  
CC bond between Asp27 and Gly28. The preferred cells for isolating murine  
CC ICE-encoding DNA include mouse macrophages and (pref.) WEHI-3 cells.  
CC Tetrapeptide aldehyde inhibitor Ac-YVAD-CHO inhibits murine ICE with a Ki  
CC of 3nM or less. This is comparable to the potency observed against the  
CC human enzyme and suggests that the active sites of both convertases are  
CC similar. Ac-YVAD-CHO was used to make an affinity ligand (Ac-YVAD-CHO)  
CC with which to purify active ICE. Due to the enzyme's unusual substrate  
CC specificity, an affinity column can be used to purify ICE in a single  
CC step from a crude cellular lysate. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX SQ Sequence 4 AA;  
Query Match 100.0%; Score 21; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
DB 1 YVAD 4

RESULT 6  
AAR77200 standard; peptide; 4 AA.  
ID AAR77200  
XX AAR77200;  
XX AAR77200;  
XX 27-FEB-1996 (first entry)  
XX Cell proliferation enzyme proteinase activity substrate peptide #5.  
DE

XX Proteinase; cell growth-stimulating protein; hydrolysis;  
KW macrophage chemotactic action; serine protease inhibitor; wound;  
KW gastric ulcer; leg ulcer; bed sore.  
XX  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
FH Modified-site 1  
FT /label= Acyl-Tyr  
FT Modified-site 4  
FT /note= "Modified by 4-methyl-coumaryl-7-amide"  
XX  
XX  
XX EP661293-A2.  
XX  
XX 05-JUL-1995.  
XX  
XX 22-DEC-1994; 94EP-00120406.  
XX  
XX 29-DEC-1993; 93JP-00351225.  
XX  
XX (SANWA ) SANWA KAGAKU KENKYUSHO CO.  
XX  
XX Yamaguchi T, Uesaka H, Watanabe K, Awaya J;  
XX WPI; 1995-233274/31.  
XX  
XX Protein derived from Clostridium perfringens FERM BP-4584 - stimulates  
FT cell proliferation and has macrophage chemotactic action.  
XX  
XX Example; Page 8; 14pp; English.  
XX  
XX The sequences given in AAR77196-200 are peptides which were used to  
CC demonstrate the proteinase activity of the cell growth-stimulating  
CC protein of the invention. The protein was seen to selectively hydrolyse  
CC synthetic substrates having an aromatic amino acid at the C-terminal. The  
CC response to the peptide given in AAR77196 was particularly high. The cell  
CC growth-stimulating protein has a mol. wt. of 420 +/- 40 kD and a single  
CC subunit mol. wt. of 130 +/- 20 kD. It has an isoelectric point of 4.8  
CC and has cell growth stimulating action and macrophage chemotactic  
CC action, as well as proteinase activity. Its enzymatic activity decreases  
CC in the presence of a serine protease inhibitor, increase in the presence  
CC of various metal ions, and is stabilised in the presence of calcium ion.  
CC The protein is particularly useful for the treatment of wounds, gastric  
CC and leg ulcers, eg. bed sores  
XX  
XX Sequence 4 AA;  
SQ  
Query Match 100.0%; Score 21; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YVAD 4  
Db 1 YVAD 4  
RESULT 7  
AAR95702  
ID AAR95702 standard; peptide; 4 AA.  
XX  
XX AAR95702;  
XX  
XX 01-AUG-1996 (first entry)  
XX  
XX Tetrapeptide aldehyde inhibitor 'Ala'.  
XX  
XX Interleukin-1-beta converting enzyme; ICE; inhibitor; inflammation;  
KW apoptosis; protein engineering; crystal structure.  
XX  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
FH

FT Modified-site 1  
FT /note= "N-terminal acetyl gp."  
XX  
XX WO9535367-A1.  
XX  
XX 28-DEC-1995.  
XX  
XX 16-JUN-1995; 95WO-US007619.  
XX  
XX 17-JUN-1994; 94US-00261582.  
XX  
XX (VERT-) VERTEX PHARM INC.  
XX  
XX Wilson KP, Griffith JP, Kim EE, Livingston DJ;  
XX WPI; 1996-058405/06.  
XX  
XX Interleukin-1 beta converting enzyme (ICE) crystal structure - useful for  
FT designing and evaluating opds., esp. inhibitors that bind to ICE active  
FT site or accessory binding site.  
XX  
XX Example 1; Page 33; 104pp; English.  
XX  
XX A tetrapeptide aldehyde (AAR95702) used in 2x molar excess completely  
CC inhibited the activity of autoprocesed interleukin-1 beta converting  
CC enzyme (ICE) (see also AAR95701) obtd. by expression of human ICE cDNA in  
CC Escherichia coli. The protein-inhibitor complex was purified, and  
CC crystals of ICE in complex with the inhibitor were grown by vapour  
CC diffusion. These were used to determine the crystal structure of ICE,  
CC useful e.g. in the design of novel ICE inhibitors  
XX  
XX Sequence 4 AA;  
SQ  
Query Match 100.0%; Score 21; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YVAD 4  
Db 1 YVAD 4  
RESULT 8  
AAR98753  
ID AAR98753 standard; peptide; 4 AA.  
XX  
XX AAR98753;  
XX  
XX 17-DEC-1996 (first entry)  
XX  
XX Asp-ase inhibitor B.  
XX  
XX Interleukin-1 beta converting enzyme; ICE; Ced-3; Asp-ase inhibitor;  
KW cell death; apoptosis; neural degeneration.  
XX  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 1  
FT /note= "N-terminal acylation"  
FT Misc-difference 4  
FT /note= "C-terminal aldehyde gp."  
XX  
XX WO9625946-A1.  
XX  
XX 29-AUG-1996.  
XX  
XX 23-FEB-1996; 96WO-US002473.  
XX  
XX 24-FEB-1995; 95US-00394189.  
XX  
XX (VASI ) MASSACHUSETTS INST TECHNOLOGY.  
XX



RELIGIONS	4, CONSERVATIVE	0, HISTORICAL	0, ANTI	0, CATHOLIC
Qy	1 YVAD 4			

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Db      1 YVAD 4
|||||
RESULT 11
AAW45979
ID      AAW45979 standard; peptide; 4 AA.
XX
XX      AC      AAW45979;
XX
XX      DT      01-JUL-1998 (first entry)
XX
XX      DE      Cysteine protease inhibiting peptide for preventing cell death.
XX
XX      KW      Neuronal cell death; neurodegenerative disorder; inhibition;
XX      KW      cysteine protease; cardiovascular; liver disease.
XX
XX      OS      Synthetic.
XX
XX      FN      WO9735876-A1.
XX
XX      PD      02-OCT-1997.
XX
XX      PF      04-MAR-1997; 97WO-US004158.
XX
XX      PR      04-MAR-1996; 96US-00610220.
XX
XX      PA      (UYCO ) UNIV COLUMBIA NEW YORK.
XX
XX      PI      Troy CM;
XX
XX      WPI; 1997-489561/45.
XX
XX      PT      New cysteine protease inhibiting peptide(s) for preventing cell death -
XX      PT      in cases of neurodegenerative, cardiovascular and liver diseases, and
XX      PT      their peptidomimetics, and general method for identifying enzyme
XX      PT      inhibiting peptides.
XX
XX      PS      Disclosure; Page 64; 112pp; English.
XX
XX      CC      This sequence is shown in the specification. The invention relates to
XX      CC      peptides of the formula: V-(AA1)n-Cys(V')-(AA2)m-V' (1), in which n and
XX      CC      m = 0-5, totalling 2-5; if n = 1, AA1 = Ala; if n = 2, (AA1)n = Gln-Ala;
XX      CC      and if n = 3 or more, (AA1)n = (X)p-Gln-Ala; X = any amino acid; p = 1-3,
XX      CC      depending on value of n; if m = 1, AA2 = Arg; if m = 2, (AA2)n = Arg-Gly;
XX      CC      if m = 3 or more, (AA2)n = Arg-Gly-(X)q; q = 1-3, depending on value of m
XX      CC      ; V, V' and V'', any or all of which may be absent, = agent able to
XX      CC      direct the compound to a specific cell. The peptides are inhibitors of
XX      CC      cysteine proteases, specifically interleukin-1 beta converting enzyme
XX      CC      (ICE). They inhibit death of cells, particularly in humans, and can be
XX      CC      used to treat neurodegenerative diseases (e.g. ageing, Alzheimer's,
XX      CC      Machado-Joseph, Parkinson's or Huntington's diseases, multiple sclerosis,
XX      CC      muscular dystrophy, stroke), cardiovascular disease and liver disorders.
XX      CC      The peptides should be more specific than pseudosubstrate inhibitors
XX
XX      SQ      Sequence 4 AA;
XX
XX      Query Match      100.0%; Score 21; DB 2; Length 4;
XX      Best Local Similarity 100.0%; Pred. No. 1.4e+06;
XX      Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY      1 YVAD 4
Db      1 YVAD 4
|||||
RESULT 13
AAW52749
ID      AAW52749 standard; peptide; 4 AA.
XX
XX      AC      AAW52749;
XX
XX      DT      02-MAR-1999 (first entry)
XX
XX      DE      Aminomethylcoumarin-substituted tetrapeptide.
XX
XX      KW      Aminomethylcoumarin; fluorescent; interleukin; ICE; caspase;
XX      KW      positional scanning synthetic combinatorial library.
XX
XX      OS      Synthetic.
XX
XX      FN      (DAND ) DANA FARBER CANCER INST INC.
XX      FN      (PROC-) PROCEPT INC.
XX
XX      PI      Reinherz E, Clayton L, Ocain TD, Patch RJ;
XX
XX      WPI; 1998-520756/44.
XX
XX      PT      Identifying agents which inhibit or enhance caspase activity - and which
XX      PT      may be used, e.g., in treatment of cancer or autoimmune diseases.
XX
XX      PS      Disclosure; Page 8; 62pp; English.
XX
XX      CC      AAW76198-W76202 are peptides used in a method for identifying an agent
XX      CC      which inhibits a caspase expressed in immature thymocytes. Such agents
XX      CC      may be used in the treatment of cancers (such as leukaemia or melanomas)
XX      CC      and autoimmune diseases. Inhibition of apoptosis can result in the
XX      CC      inhibition of lymphocyte down regulation, resulting in a T cell receptor
XX      CC      population with an increased proportion of autoreactive T cells, i.e., an
XX      CC      increased occurrence of T cells which have specificity for the host
XX      CC      animal's own cells (e.g. cancer cells). By the same token, increasing the
XX      CC      activity of the caspase enzyme enhances apoptosis of self-recognising T
XX      CC      cells, resulting in a decrease in the population of T cells which are
XX      CC      responsible for autoimmune disorders. The compounds may also be useful in
XX      CC      treating infections, inflammatory diseases and neurodegenerative
XX      CC      disorders
XX
XX      SQ      Sequence 4 AA;
XX
XX      Query Match      100.0%; Score 21; DB 2; Length 4;
XX      Best Local Similarity 100.0%; Pred. No. 1.4e+06;
XX      Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY      1 YVAD 4
Db      1 YVAD 4
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RESULT 12
AAW76199
ID      AAW76199 standard; protein; 4 AA.
XX
XX      AC      AAW76199;
XX
XX      DT      26-NOV-1998 (first entry)
XX
XX      FN      (first entry)
XX
XX      PT      Note= "the N-terminal is acetylated"

```

```

PR 11-OCT-1996; 96US-0028313P.
XX (WARN ) WARNER LAMBERT CO.
XX PA
XX PI
XX PI Albrecht HP, Allen HJ, Brady XD, Harter WG, Kostian CR, Roth BD;
XX PI Walker N;
XX DR WPI; 1998-312002/27.
XX PT New sulphonamide compounds - are inhibitors of interleukin-beta
XX PT converting enzyme and caspase-4, used for treating stroke and
XX PT inflammatory diseases, etc.
XX PS
XX PS Example 6; Page 35; 56pp; English.
XX CC The invention provides sulphonamide compounds of specified formula and
XX CC their salts, esters, amides and prodrugs. The sulphonamide compounds are
XX CC used for inhibiting interleukin beta converting enzyme (ICE), inhibiting
XX CC caspase-4, treating or preventing stroke, inflammatory diseases e.g.
XX CC arthritis, inflammatory bowel disease, septic shock, reperfusion injury,
XX CC Alzheimer's disease and shigellosis. The present sequence represents a
XX CC peptide substrate specific for ICE
XX SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 YVAD 4
   ||||
Db 1 YVAD 4

RESULT 15
AAW56304
ID AAW56304 standard; peptide; 4 AA.
XX AC
XX AC AAW56304;

```

DT	22-JUL-1998	(first entry)
DE	Peptide cleaved by interleukin-1-beta-converting enzyme-like protein.	
DE	XX	
KW	N-acetyl-YVAD-methyl coumarinamide; MCA;	
KW	interleukin-1- beta converting enzyme-like activity; ICE activity;	
KW	cysteine protease; investigation; substrate specificity.	
XX	Synthetic.	
OS	XX	
PN	JP10099075-A.	
XX	XX	
PD	21-APR-1998.	
XX	XX	
PF	30-SEP-1996; 96JP-00276813.	
XX	XX	
PR	30-SEP-1996; 96JP-00276813.	
XX	XX	
PA	(SHIS ) SHISEIDO CO LTD.	
XX	XX	
DR	WPI; 1998-289868/26.	
XX	XX	
PT	Protein with interleukin-1-beta converting enzyme-like activity - useful	
PT	in investigation of substrate specificity in, e.g. Parkinson's disease.	
XX	XX	
PS	Disclosure; Page 2; 5pp; Japanese.	
XX	XX	
CC	The present sequence, N-acetyl-YVAD-methyl coumarinamide (MCA),	
CC	represents a sequence that is cleaved by a protein with interleukin-1-	
CC	beta converting enzyme (ICE)-like activity. The protein, which is	
CC	obtained from human keratinocytes, has a relative molecular weight of 80	
CC	kDa. The ICE protein is part of the cysteine protease family and is	
CC	useful for investigation of the mechanism of substrate specificity (e.g.	
CC	XX	

CC Alzheimer's disease, Parkinson's disease, autoimmune disease, lymphoma,  
CC cancer and apoptosis)  
XX  
SQ Sequence 4 AA;  
  
Query Match 100.0%; Score 21; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. NO. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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    |  
    |  
Db 1 YVAD 4  
  
Search completed: May 24, 2004, 14:38:15  
Job time : 53 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 24, 2004, 14:36:17 ; Search time 16.5 Seconds  
(without alignments)  
12.515 Million cell updates/sec

Title: US-09-765-105A-1

Perfect score: 21

Sequence: 1 YVAD 4

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*

1: /cgn2\_6/ptodata/2/iaa/5A COMB.pcp.\*

2: /cgn2\_6/ptodata/2/iaa/5B COMB.pcp.\*

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4: /cgn2\_6/ptodata/2/iaa/6B COMB.pcp.\*

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6: /cgn2\_6/ptodata/2/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	4	1 US-08-354-685-1	Sequence 1, Appli
2	21	100.0	4	1 US-08-446-925-10	Sequence 10, Appl
3	21	100.0	4	1 US-08-464-964-1	Sequence 1, Appli
4	21	100.0	4	1 US-08-464-964-2	Sequence 2, Appli
5	21	100.0	4	1 US-08-700-716-1	Sequence 1, Appli
6	21	100.0	4	1 US-08-700-716-16	Sequence 16, Appl
7	21	100.0	4	1 US-08-592-029-4	Sequence 4, Appli
8	21	100.0	4	1 US-08-592-029-5	Sequence 5, Appli
9	21	100.0	4	1 US-08-777-208-8	Sequence 8, Appli
10	21	100.0	4	2 US-08-800-007A-11	Sequence 11, Appl
11	21	100.0	4	2 US-08-440-898-1	Sequence 2, Appli
12	21	100.0	4	2 US-08-440-898-2	Sequence 2, Appli
13	21	100.0	4	2 US-09-067-053-1	Sequence 1, Appli
14	21	100.0	4	2 US-09-067-053-16	Sequence 16, Appl
15	21	100.0	4	2 US-09-146-331-10	Sequence 10, Appl
16	21	100.0	4	2 US-08-394-189B-16	Sequence 16, Appl
17	21	100.0	4	2 US-08-394-189B-17	Sequence 17, Appl
18	21	100.0	4	2 US-08-828-941A-1	Sequence 1, Appli
19	21	100.0	4	2 US-08-828-941A-2	Sequence 2, Appli
20	21	100.0	4	2 US-08-883-632-4	Sequence 4, Appli
21	21	100.0	4	2 US-08-883-632-5	Sequence 5, Appli
22	21	100.0	4	2 US-08-915-414A-2	Sequence 2, Appli
23	21	100.0	4	2 US-08-592-013A-4	Sequence 4, Appli
24	21	100.0	4	2 US-08-592-013A-5	Sequence 5, Appli
25	21	100.0	4	2 US-08-896-885-10	Sequence 10, Appl
26	21	100.0	4	2 US-08-712-878-1	Sequence 1, Appli
27	21	100.0	4	2 US-08-712-878-8	Sequence 8, Appli

28 21 100.0 4 2 US-08-712-878-9 Sequence 9, Appli

29 21 100.0 4 3 US-08-465-216-1 Sequence 1, Appli

30 21 100.0 4 3 US-08-465-216-2 Sequence 2, Appli

31 21 100.0 4 3 US-09-017-276-1 Sequence 1, Appli

32 21 100.0 4 3 US-08-761-483-1 Sequence 1, Appli

33 21 100.0 4 3 US-08-761-483-2 Sequence 2, Appli

34 21 100.0 4 3 US-08-761-483-5 Sequence 5, Appli

35 21 100.0 4 3 US-08-761-483-6 Sequence 6, Appli

36 21 100.0 4 3 US-08-761-483-11 Sequence 11, Appli

37 21 100.0 4 3 US-09-058-969-3 Sequence 3, Appli

38 21 100.0 4 3 US-09-130-193-3 Sequence 3, Appli

39 21 100.0 4 3 US-09-357-952-2 Sequence 2, Appli

40 21 100.0 4 3 US-09-309-003-2 Sequence 2, Appli

41 21 100.0 4 3 US/08/869 Sequence 2, Appli

42 21 100.0 4 3 US-09-257-218-83 Sequence 83, Appli

43 21 100.0 4 3 US-09-311-760-83 Sequence 83, Appli

44 21 100.0 4 3 US-09-291-692-72 Sequence 72, Appli

45 21 100.0 4 3 US-08-665-643A-44 Sequence 44, Appli

#### ALIGNMENTS

RESULT 1

US-08-354-685-1

; Sequence 1, Application US/08354685

; Patent No. 5498695

; GENERAL INFORMATION:

; APPLICANT: Daumy, Gaston O.

; APPLICANT: Reiter, Lawrence A.

; TITLE OF INVENTION: PARA-NITROANILIDE PEPTIDES

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dr. Peter C. Richardson

; STREET: 235 East 42nd Street, 20th Floor

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10017-5755

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/354,685

; FILING DATE:

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 981,153

; FILING DATE: 24-NOV-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Strassburger, Philip C.

; REGISTRATION NUMBER: 34,258

; REFERENCE/DOCKET NUMBER: PC8352

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)573-5731

; TELEFAX: (212)573-1939

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

US-08-354-685-1

Query Match 100.0%; Score 21; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4



APPLICANT: Livingston, David J  
TITLE OF INVENTION: INHIBITORS OF INTERLEUKIN-1 BETA  
TITLE OF INVENTION: CONVERTING ENZYME  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr.  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,964  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/440,898  
FILING DATE: 25-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/405,581  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/261,452  
FILING DATE: 17-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr, James F  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: VPI/94-04 CIPRI DIVI  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /product= "OTHER"  
OTHER INFORMATION: /note= "tyrosine is acetylated"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 4  
OTHER INFORMATION: /product= "OTHER"  
OTHER INFORMATION: /note= "aspartic acid is derivatized with  
amino-4-methylcoumarin"  
US-08-464-964-2

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
Db 1 YVAD 4

RESULT 5  
US-08-700-716-1  
Sequence 1, Application US/08700716  
Patent No. 5744451  
GENERAL INFORMATION:  
APPLICANT: Allen, Hamish J

APPLICANT: Banerjee, Subhashis  
APPLICANT: Brady, Kenneth D  
APPLICANT: Hodges, John C  
APPLICANT: Kostlan, Catherine R  
APPLICANT: Talanian, Robert V  
TITLE OF INVENTION: N-Substituted Glutamic Acid Derivatives  
TITLE OF INVENTION: with Interleukin-1 Converting Enzyme Inhibitory Activity  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Elizabeth M. Anderson  
STREET: 2800 Plymouth Road  
CITY: Ann Arbor  
STATE: MI  
COUNTRY: US  
ZIP: 48105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Ver 1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/700,716  
FILING DATE: 13-AUG-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Anderson, Elizabeth M  
REGISTRATION NUMBER: 31585  
REFERENCE/DOCKET NUMBER: PD-5363-01-EMA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 313 996-7304  
TELEFAX: 313 996-1553  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-700-716-1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
Db 1 YVAD 4

RESULT 6  
US-08-700-716-16  
Sequence 16, Application US/08700716  
Patent No. 5744451  
GENERAL INFORMATION:  
APPLICANT: Allen, Hamish J  
APPLICANT: Banerjee, Subhashis  
APPLICANT: Brady, Kenneth D  
APPLICANT: Hodges, John C  
APPLICANT: Kostlan, Catherine R  
APPLICANT: Talanian, Robert V  
TITLE OF INVENTION: N-Substituted Glutamic Acid Derivatives  
TITLE OF INVENTION: with Interleukin-1 Converting Enzyme Inhibitory Activity  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Elizabeth M. Anderson  
STREET: 2800 Plymouth Road  
CITY: Ann Arbor  
STATE: MI  
COUNTRY: US  
ZIP: 48105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Ver 1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/700,716  
FILING DATE: 13-AUG-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Anderson, Elizabeth M  
REGISTRATION NUMBER: 31585  
REFERENCE/DOCKET NUMBER: PD-5363-01-EMA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 313 996-7304  
TELEFAX: 313 996-1553  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-700-716-16

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|  
|  
|  
Db 1 YVAD 4

RESULT 7  
US-08-592-029-4  
Sequence 4, Application US/08592029  
Patent No. 5763196  
GENERAL INFORMATION:  
APPLICANT: POWELL, MICHAEL J.  
APPLICANT: KHANNA, PYARE  
APPLICANT: LINGENFELTER, DAVID  
APPLICANT: EISENBEIS, SCOTT J.  
TITLE OF INVENTION: ASSAYS USING CROSS-LINKED POLYPEPTIDE  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/592,029  
FILING DATE: 26-JAN-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MONROY, GLADYS H.  
REGISTRATION NUMBER: 32,430  
REFERENCE/DOCKET NUMBER: 33746-20004.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141 MRSNFOERS SFO  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 4  
OTHER INFORMATION: /product= "OTHER"  
OTHER INFORMATION: /label= Asp-NH-CH3  
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NAME/KEY: Modified-site  
LOCATION: 1  
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US-08-592-029-4  
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Best Local Similarity 100.0%; Pred. No. 3e+05;  
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QY 1 YVAD 4  
|  
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|  
|  
Db 1 YVAD 4  
|  
|  
|  
|  
RESULT 8  
US-08-592-029-5  
Sequence 5, Application US/08592029  
Patent No. 5763196  
GENERAL INFORMATION:  
APPLICANT: POWELL, MICHAEL J.  
APPLICANT: KHANNA, PYARE  
APPLICANT: LINGENFELTER, DAVID  
APPLICANT: EISENBEIS, SCOTT J.  
TITLE OF INVENTION: ASSAYS USING CROSS-LINKED POLYPEPTIDE  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/592,029  
FILING DATE: 26-JAN-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MONROY, GLADYS H.  
REGISTRATION NUMBER: 32,430  
REFERENCE/DOCKET NUMBER: 33746-20004.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141 MRSNFOERS SFO  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 4  
OTHER INFORMATION: /note= "chloromethylketone group  
OTHER INFORMATION: attached"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1



OTHER INFORMATION: /product= "OTHER"  
OTHER INFORMATION: /label= Ac-Tyr  
OTHER INFORMATION: /note= "Acetyl tyrosine"  
US-08-592-029-5

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4  
Db 1 YVAD 4

#### RESULT 9

US-08-777-208-8  
Sequence 8, Application US/08777208  
Patent No. 5763576  
GENERAL INFORMATION:  
APPLICANT: Powers, James C.  
TITLE OF INVENTION: Tetrapeptide Alpha-Ketoamides  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Deveau, Colton & Marquis  
STREET: Two Midtown Plaza, Suite 1400  
CITY: Atlanta  
STATE: GA  
COUNTRY: USA  
ZIP: 30309

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Microsoft Windows 95  
SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/777,208  
FILING DATE: 27-DEC-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/539944  
FILING DATE: 06-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Colton, Laurence P.  
REGISTRATION NUMBER: 33371  
REFERENCE/DOCKET NUMBER: 10733-191B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404) 875-3555  
TELEFAX: (404) 875-8505  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: no

US-08-777-208-8

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4  
Db 1 YVAD 4

#### RESULT 10

US-08-800-007A-11  
Sequence 11, Application US/08800007A  
Patent No. 5834228  
GENERAL INFORMATION:  
APPLICANT: Becker, Joseph  
ADDRESSEE: Nicholson, Donald

APPLICANT: Rtoroda, Jennifer  
APPLICANT: Thornberry, Nancy  
APPLICANT: Fazil, Kimberly  
APPLICANT: Gallant, Michel  
APPLICANT: Gareau, Yves  
APPLICANT: Labelle, Marc  
APPLICANT: Peterson, Erin  
APPLICANT: Rasper, Dita  
TITLE OF INVENTION: CRYSTAL STRUCTURE OF APOPAIN  
TITLE OF INVENTION: AND USES THEREOF  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JOSEPH A. COPPOLA - MERCK & CO., INC.  
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000  
CITY: RAHWAY  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/800,007A  
FILING DATE: 13-FEB-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: COPPOLA, JOSEPH A  
REGISTRATION NUMBER: 38,413  
REFERENCE/DOCKET NUMBER: 19644  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-6734  
TELEFAX: 732-594-4720

TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-800-007A-11

Query Match 100.0%; Score 21; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4  
Db 1 YVAD 4

#### RESULT 11

US-08-440-898-1  
Sequence 1, Application US/08440898  
Patent No. 5847135  
GENERAL INFORMATION:  
APPLICANT: Bemis, Guy W  
APPLICANT: Golec, Julian M.C.  
APPLICANT: Laufer, David J  
APPLICANT: Mullican, Michael D  
APPLICANT: Murcko, Mark A  
APPLICANT: Livingston, David J  
TITLE OF INVENTION: INHIBITORS OF INTERLEUKIN-1  
TITLE OF INVENTION: BETA CONVERTING ENZYME  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr.  
STREET: 1251 Avenue of the Americas

STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/440,898  
FILING DATE: 25-MAY-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/405,581  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/261,452  
FILING DATE: 17-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr, James F  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: VPI/94-04 CIPRI DIVI  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /product= "OTHER"  
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FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 4  
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US-08-440-898-1  
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Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 YVAD 4  
Db 1 YVAD 4  
RESULT 12  
US-08-440-898-2  
Sequence 2, Application US/08440898  
Patent No. 5847135  
GENERAL INFORMATION:  
APPLICANT: Bemis, Guy W  
APPLICANT: Golec, Julian M.C.  
APPLICANT: Lauffer, David J  
APPLICANT: Mullican, Michael D  
APPLICANT: Murcko, Mark A  
APPLICANT: Livingston, David J  
TITLE OF INVENTION: INHIBITORS OF INTERLEUKIN-1  
TITLE OF INVENTION: BETA CONVERTING ENZYME  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr.

STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/440,898  
FILING DATE: 25-MAY-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/405,581  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/261,452  
FILING DATE: 17-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr, James F  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: VPI/94-04 CIPRI DIVI  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: Modified-site  
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US-08-440-898-2  
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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 YVAD 4  
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US-08-067-053-1  
Sequence 1, Application US/09067053  
Patent No. 5932549  
GENERAL INFORMATION:  
APPLICANT: Allen, Hamish J  
APPLICANT: Banerjee, Subhashis  
APPLICANT: Brady, Kenneth D  
APPLICANT: Hodges, John C  
APPLICANT: Kostian, Catherine R  
APPLICANT: Talianian, Robert V  
TITLE OF INVENTION: N-Substituted Glutamic Acid Derivatives  
TITLE OF INVENTION: with Interleukin-1 Converting Enzyme Inhibitory Activity  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Elizabeth M. Anderson  
STREET: 2800 Plymouth Road  
CITY: Ann Arbor  
STATE: MI  
COUNTRY: US  
ZIP: 48105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Ver 1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/067,053  
FILING DATE: 27-APR-1998  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/700,716  
FILING DATE: 13-AUG-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Anderson, Elizabeth M  
REGISTRATION NUMBER: 31585  
REFERENCE/DOCKET NUMBER: PD-5363-01-EVA  
TELEPHONE: 313 996-7304  
TELEFAX: 313 996-7304  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-067-053-1

Query Match 100.0%; Score 21; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YVAD 4  
DB 1 YVAD 4

RESULT 14  
US-09-067-053-16  
Sequence 16, Application US/09067053  
Patent No. 5932549  
GENERAL INFORMATION:  
APPLICANT: Allen, Hamish J  
APPLICANT: Banerjee, Subhashis  
APPLICANT: Brady, Kenneth D  
APPLICANT: Hodges, John C  
APPLICANT: Kostlan, Catherine R  
APPLICANT: Talanian, Robert V  
TITLE OF INVENTION: N-Substituted Glutamic Acid Derivatives  
TITLE OF INVENTION: with Interleukin-1 Converting Enzyme Inhibitory Activity  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Elizabeth M. Anderson  
STREET: 2800 Plymouth Road  
CITY: Ann Arbor  
STATE: MI  
COUNTRY: US  
ZIP: 48105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Ver 1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/067,053  
FILING DATE: 27-APR-1998

LISTING DVT-  
758100  
G089

CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/700,716  
FILING DATE: 13-AUG-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Anderson, Elizabeth M  
REGISTRATION NUMBER: 31585  
REFERENCE/DOCKET NUMBER: PD-5363-01-EVA  
TELEPHONE: 313 996-7304  
TELEFAX: 313 996-1553  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-067-053-16  
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Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YVAD 4  
DB 1 YVAD 4  
RESULT 15  
US-09-746-331-10  
Sequence 10, Application US/09146331  
Patent No. 5958720  
GENERAL INFORMATION:  
APPLICANT: Ittack, Gerald  
APPLICANT: Altmari, Smad S.  
APPLICANT: Fernandez-Alnemri, Teresa  
TITLE OF INVENTION: Mch2, AN APOPTOTIC CYSTEINE  
PROTEASE, AND COMPOSITIONS FOR MAKING AND  
TITLE OF INVENTION: METHODS OF USING THE SAME  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &  
ADDRESSEE: No. 5958720ris  
STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/146,331  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/896,885  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: T0U-1508  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-146-331-10
Query Match      100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 YVAD 4

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Job time : 16.5 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 24, 2004, 14:39:37 ; Search time 38 Seconds  
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29.360 Million cell updates/sec

Title: US-09-765-105A-1

Perfect score: 21  
Sequence: 1 YVAD 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1149313 seqs, 278921704 residues 1149313

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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SUMMARIES

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2	21	100.0	4	9	US-09-799-463-3
3	21	100.0	4	9	US-09-735-363A-84
4	21	100.0	4	9	US-09-799-994-3
5	21	100.0	4	9	US-09-952-768-72
6	21	100.0	4	9	US-09-150-623-7
7	21	100.0	4	9	US-09-858-754-10
8	21	100.0	4	9	US-09-987-417-2
9	21	100.0	4	9	US-09-977-831-35
10	21	100.0	4	9	US-09-888-243-17
11	21	100.0	4	9	US-09-947-387-2
12	21	100.0	4	9	US-09-964-114-3
13	21	100.0	4	9	US-09-964-114-4
14	21	100.0	4	9	US-09-964-114-6
15	21	100.0	4	10	US-09-161-172-1

16	21	100.0	4	12	US-10-668-955-72	Sequence 72, Appl
17	21	100.0	4	12	US-09-746-731-83	Sequence 83, Appl
18	21	100.0	4	12	US-09-765-105-1	Sequence 1, Appl
19	21	100.0	4	12	US-09-795-651-13	Sequence 13, Appl
20	21	100.0	4	12	US-09-863-649-1	Sequence 1, Appl
21	21	100.0	4	12	US-09-270-983-7	Sequence 7, Appl
22	21	100.0	4	12	US-10-099-408A-1	Sequence 1, Appl
23	21	100.0	4	12	US-09-973-476-2	Sequence 2, Appl
24	21	100.0	4	12	US-10-356-665-2	Sequence 2, Appl
25	21	100.0	4	13	US-10-103-448-7	Sequence 7, Appl
26	21	100.0	4	13	US-10-059-749-83	Sequence 83, Appl
27	21	100.0	4	13	US-10-108-929-7	Sequence 7, Appl
28	21	100.0	4	14	US-10-171-077-10	Sequence 10, Appl
29	21	100.0	4	14	US-10-165-015-35	Sequence 35, Appl
30	21	100.0	4	14	US-10-105-779-2	Sequence 2, Appl
31	21	100.0	4	14	US-10-123-529-26	Sequence 26, Appl
32	21	100.0	4	14	US-10-123-529-28	Sequence 28, Appl
33	21	100.0	4	14	US-10-337-169-27	Sequence 27, Appl
34	21	100.0	4	14	US-10-337-169-30	Sequence 30, Appl
35	21	100.0	4	14	US-10-337-060-16	Sequence 16, Appl
36	21	100.0	4	14	US-10-302-811-3	Sequence 3, Appl
37	21	100.0	4	14	US-10-322-361-1	Sequence 1, Appl
38	21	100.0	4	15	US-10-138-375-2	Sequence 2, Appl
39	21	100.0	4	15	US-10-341-979-12	Sequence 12, Appl
40	21	100.0	5	8	US-08-610-220A-6	Sequence 6, Appl
41	21	100.0	5	9	US-09-150-623-6	Sequence 6, Appl
42	21	100.0	5	9	US-09-954-897-40	Sequence 40, Appl
43	21	100.0	5	9	US-09-947-387-72	Sequence 72, Appl
44	21	100.0	5	10	US-09-997-463B-5	Sequence 5, Appl
45	21	100.0	5	13	US-10-057-505-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1  
US-08-610-220A-7  
; Sequence 7, Application US/08610220A  
; Publication No. US20030099638A1  
; GENERAL INFORMATION:  
; APPLICANT: TROY, Carol M.  
; TITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL  
; TITLE OF INVENTION: DEATH AND USES THEREOF  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/610,220A  
; FILING DATE: MAR-04-1996  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 48332/JPW/JML  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

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; MOLECULE TYPE: peptide
US-08-610-220A-7
Query Match      100.0%; Score 21; DB 8; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YVAD 4
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Db      1 YVAD 4

RESULT 2
US-09-799-463-3
; Sequence 3, Application US/09799463
; Patent No. US20010018195A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Deveraux, Quinn
; APPLICANT: Salvessen, Guy S.
; APPLICANT: Takahashi, Ryosuke
; APPLICANT: Roy, Natalie
; TITLE OF INVENTION: Screening Assays For Agents That Alter Inhibitor of
; FILE REFERENCE: LJ 3080
; CURRENT APPLICATION NUMBER: US/09/799,463
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 09/058,969
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 08/862,087
; PRIOR FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Consensus Sequence
US-09-799-463-3
Query Match      100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YVAD 4
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Db      1 YVAD 4

RESULT 3
US-09-735-363A-84
; Sequence 84, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Fillon, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 84
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide

US-09-735-363A-84
Query Match      100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YVAD 4
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Db      1 YVAD 4

RESULT 4
US-09-799-994-3
; Sequence 3, Application US/09799994
; Patent No. US20020009757A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Deveraux, Quinn
; APPLICANT: Salvessen, Guy S.
; APPLICANT: Takahashi, Ryosuke
; APPLICANT: Roy, Natalie
; TITLE OF INVENTION: Apoptosis (IAP) Protein Regulation of Caspase Activity
; FILE REFERENCE: LJ 3080
; CURRENT APPLICATION NUMBER: US/09/799,994
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 09/058,969
; PRIOR FILING DATE: 1998-04-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Consensus Sequence
US-09-799-994-3
Query Match      100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YVAD 4
      ||||
Db      1 YVAD 4

RESULT 5
US-09-952-768-72
; Sequence 72, Application US/09952768
; Patent No. US20020035242A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,
; FILE REFERENCE: NUCLEIC ACIDS ENCODING AND METHODS OF USE
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: Suite 6300, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/09/952,768  
FILING DATE: 10-Sep-2001  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Christiansen, William T.  
REGISTRATION NUMBER: 44,614  
REFERENCE/DOCKET NUMBER: 480140.424C4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 72:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 72:

US-09-952-768-72

Query Match 100.0%; Score 21; DB 9; Length 4;  
Best Local Similarity 100.0%; Pred. NO. 1e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
DB 1 YVAD 4

## RESULT 6

US-09-150-623-7  
Sequence 7, Application US/09150623  
Patent No. US20020044931A1  
GENERAL INFORMATION:  
APPLICANT: Troy, Carol M.  
TITLE OF INVENTION: COMPOUNDS WHICH PREVENT NEURONAL CELL  
TITLE OF INVENTION: DEATH AND USES THEREOF  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/150,623  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/610,220  
FILING DATE: MAR-04-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 48332/JPW/JML  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0525  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-09-150-623-7

Query Match 100.0%; Score 21; DB 9; Length 4;

Best Local Similarity 100.0%; Pred. NO. 1e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
DB 1 YVAD 4

## RESULT 7

US-09-858-754-10  
Sequence 10, Application US/09858754  
Patent No. US20020055130A1  
GENERAL INFORMATION:  
APPLICANT: Johnson, Gary L.  
TITLE OF INVENTION: METHOD AND PRODUCT FOR REGULATING APOPTOSIS  
FILE REFERENCE: CPI-042  
CURRENT APPLICATION NUMBER: US/09/858,754  
CURRENT FILING DATE: 2001-05-16  
PRIOR APPLICATION NUMBER: 09/023,130  
PRIOR FILING DATE: 1998-02-13  
PRIOR APPLICATION NUMBER: 60/039,740  
PRIOR FILING DATE: 1997-02-14  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patent in Ver. 2.0  
SEQ ID NO 10  
LENGTH: 4  
TYPE: PPT  
ORGANISM: synthetic construct  
US-09-858-754-10

Query Match 100.0%; Score 21; DB 9; Length 4;  
Best Local Similarity 100.0%; Pred. NO. 1e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
DB 1 YVAD 4

## RESULT 8

US-09-987-417-2  
Sequence 2, Application US/09987417  
Patent No. US20020058631A1  
GENERAL INFORMATION:  
APPLICANT: Cai, Sui Xiong  
APPLICANT: Weber, Eckard  
APPLICANT: Wang, Yan  
APPLICANT: Mills, Gordon B.  
APPLICANT: Green, Douglas R.  
TITLE OF INVENTION: Caspase Inhibitors and the Use Thereof  
FILE REFERENCE: 1735.0350003  
CURRENT APPLICATION NUMBER: US/09/987,417  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 09/545,565  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: US 60/128,545  
PRIOR FILING DATE: 1999-04-09  
PRIOR APPLICATION NUMBER: US 60/158,370  
PRIOR FILING DATE: 1999-10-12  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO 2  
LENGTH: 4  
TYPE: PPT  
ORGANISM: Unknown Organism  
FEATURE:  
OTHER INFORMATION: caspase-1 inhibitor  
US-09-987-417-2

Query Match 100.0%; Score 21; DB 9; Length 4;  
Best Local Similarity 100.0%; Pred. NO. 1e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4  
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Db 1 YVAD 4

## RESULT 9

US-09-977-831-35  
; Sequence 35, Application US/09977831  
; Patent No. US20020120100A1  
; GENERAL INFORMATION:  
; APPLICANT: PACTT, Tech Transfer Office University of Lausanne  
; APPLICANT: Bonny, Christophe  
; TITLE OF INVENTION: INTRACELLULAR DELIVERY OF BIOLOGICAL EFFECTORS  
; FILE REFERENCE: 20349-512 Transporter peptides  
; CURRENT APPLICATION NUMBER: US/09/977,831  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/240,315  
; PRIOR FILING DATE: 2000-10-13  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 35  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Caspase  
; OTHER INFORMATION: Inhibitor peptide  
US-09-977-831-35

Query Match 100.0%; Score 21; DB 9; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4  
|||||  
Db 1 YVAD 4

## RESULT 10

US-09-888-243-17  
; Sequence 17, Application US/09888243  
; Patent No. US20020136714A1  
; GENERAL INFORMATION:  
; APPLICANT: Horvitz, H. Robert  
; APPLICANT: Yuan, Junying  
; APPLICANT: Shaham, Shai  
; TITLE OF INVENTION: Relatedness of Human Interleukin-lbета  
; TITLE OF INVENTION: Convertase Gene to a C. Elegans Cell Death Gene, Inhibitory  
; TITLE OF INVENTION: Portions of these Genes and Uses Therefor  
; FILE REFERENCE: 01997/211003  
; CURRENT APPLICATION NUMBER: US/09/888,243  
; CURRENT FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: US 09/083,662  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: US 08/394,189  
; PRIOR FILING DATE: 1995-02-24  
; PRIOR APPLICATION NUMBER: US 08/282,211  
; PRIOR FILING DATE: 1994-07-11  
; PRIOR APPLICATION NUMBER: US 07/984,182  
; PRIOR FILING DATE: 1992-11-20  
; PRIOR APPLICATION NUMBER: US 07/897,788  
; PRIOR FILING DATE: 1992-06-12  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Designed Peptide  
US-09-888-243-17

Query Match 100.0%; Score 21; DB 9; Length 4;

Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4  
|||||  
Db 1 YVAD 4

## RESULT 11

US-09-947-387-2  
; Sequence 2, Application US/09947387  
; Patent No. US20020150885A1  
; GENERAL INFORMATION:  
; APPLICANT: Weber, Eckard  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Keana, John F.W.  
; APPLICANT: Drewe, John A.  
; APPLICANT: Zhang, Han-Zhong  
; TITLE OF INVENTION: No. US20020150885A1el Fluorogenic or Fluorescent Reporter Molecu  
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence  
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the  
; TITLE OF INVENTION: Use thereof  
; FILE REFERENCE: 1735.0290005  
; CURRENT APPLICATION NUMBER: US/09/947,387  
; CURRENT FILING DATE: 2001-09-07  
; PRIOR APPLICATION NUMBER: US 60/061,582  
; PRIOR FILING DATE: 1997-10-10  
; PRIOR APPLICATION NUMBER: US 60/145,746  
; PRIOR FILING DATE: 1998-03-03  
; PRIOR APPLICATION NUMBER: US 09/168,888  
; PRIOR FILING DATE: 1998-10-09  
; NUMBER OF SEQ ID NOS: 142  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-947-387-2

Query Match 100.0%; Score 21; DB 9; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4  
|||||  
Db 1 YVAD 4

## RESULT 12

US-09-964-114-3  
; Sequence 3, Application US/09964114  
; Patent No. US20020156094A1  
; GENERAL INFORMATION:  
; APPLICANT: Albrecht, Hans P. et al.  
; TITLE OF INVENTION: Sulfonamide Interleukin-lbета Converting Enzyme  
; TITLE OF INVENTION: Inhibitors  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/964,114  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 09/284,422  
; PRIOR FILING DATE: 1999-04-02  
; PRIOR APPLICATION NUMBER: PCT/US97/18396  
; PRIOR FILING DATE: 1999-10-09  
; PRIOR APPLICATION NUMBER: 60/028,313  
; PRIOR FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 4  
; TYPE: PRT  
US-09-964-114-3

Query Match 100.0%; Score 21; DB 9; Length 4;



ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: UNSURE  
LOCATION: (1)..(4)  
OTHER INFORMATION: Acetyl group attached to 5' end and AMC group  
OTHER INFORMATION: attached to 3' end  
OTHER INFORMATION: Description of Artificial Sequence: Chemically  
OTHER INFORMATION: synthesized  
US-09-964-114-3

Query Match 100.0%; Score 21; DB 9; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
|||  
Db 1 YVAD 4

RESULT 13  
US-09-964-114-4  
Sequence 4, Application US/09964114  
Patent No. US20020156094A1  
GENERAL INFORMATION:  
APPLICANT: Albrecht, Hans P. et al.  
TITLE OF INVENTION: Sulfonamide Interleukin-1Beta Converting Enzyme  
TITLE OF INVENTION: Inhibitors  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/09/964,114  
CURRENT FILING DATE: 2001-09-25  
PRIOR APPLICATION NUMBER: 09/284,422  
PRIOR FILING DATE: 1999-04-02  
PRIOR APPLICATION NUMBER: PCT/US97/18396  
PRIOR FILING DATE: 1999-10-09  
PRIOR APPLICATION NUMBER: 60/028,313  
PRIOR FILING DATE: 1998-10-11  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 4  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: UNSURE  
LOCATION: (1)..(4)  
OTHER INFORMATION: Acetyl group attached to 5' end and pNA group  
OTHER INFORMATION: attached to 3' end  
OTHER INFORMATION: Description of Artificial Sequence: Chemically  
OTHER INFORMATION: synthesized  
US-09-964-114-4

Query Match 100.0%; Score 21; DB 9; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
|||  
Db 1 YVAD 4

RESULT 14  
US-09-964-114-6  
Sequence 6, Application US/09964114  
Patent No. US20020156094A1  
GENERAL INFORMATION:  
APPLICANT: Albrecht, Hans P. et al.  
TITLE OF INVENTION: Sulfonamide Interleukin-1Beta Converting Enzyme  
TITLE OF INVENTION: Inhibitors  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/09/964,114  
CURRENT FILING DATE: 2001-09-25  
PRIOR APPLICATION NUMBER: 09/284,422  
PRIOR FILING DATE: 1999-04-02

PRIOR APPLICATION NUMBER: PCT/US97/18396  
PRIOR FILING DATE: 1999-10-09  
PRIOR APPLICATION NUMBER: 60/028,313  
PRIOR FILING DATE: 1996-10-11  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 6  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: UNSURE  
LOCATION: (1)..(4)  
OTHER INFORMATION: Acetyl group attached to 5' end and pNA group  
OTHER INFORMATION: attached to 3' end  
OTHER INFORMATION: Description of Artificial Sequence: Chemically  
OTHER INFORMATION: synthesized  
US-09-964-114-6

Query Match 100.0%; Score 21; DB 9; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
|||  
Db 1 YVAD 4

RESULT 15  
US-09-161-172-1  
Sequence 1, Application US/09161172  
Publication No. US2003004476A1  
GENERAL INFORMATION:  
APPLICANT: Dykens, James A.  
APPLICANT: Miller, Scott W.  
APPLICANT: Ghosh, Soumitra S.  
APPLICANT: Davis, Robert E.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING  
TITLE OF INVENTION: AGENTS THAT ALTER MITOCHONDRIAL PERMEABILITY  
TITLE OF INVENTION: TRANSITION PORES  
FILE REFERENCE: 660088.418  
CURRENT APPLICATION NUMBER: US/09/161,172  
CURRENT FILING DATE: 1998-09-25  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: caspase-1 specific fluorogenic peptide substrate  
US-09-161-172-1

Query Match 100.0%; Score 21; DB 10; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
|||  
Db 1 YVAD 4

Search completed: May 24, 2004, 14:49:50  
Job time : 39 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 24, 2004, 14:38:22 ; Search time 175 Seconds  
(without alignments)  
22.310 Million cell updates/sec

Title: US-09-765-105A-1

Perfect score: 21

Sequence: 1 YVAD 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6019581 seqs, 976053577 residues

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Minimum DB seq length: 0

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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3	21	100.0	4	1	PCT-US01-04137-3	Sequence 3, Appli
4	21	100.0	4	1	PCT-US02-18014-9	Sequence 9, Appli
5	21	100.0	4	1	PCT-US02-18484-9	Sequence 9, Appli
6	21	100.0	4	1	PCT-US02-37577-3	Sequence 3, Appli
7	21	100.0	4	1	PCT-US03-20997-7	Sequence 7, Appli
8	21	100.0	4	1	PCT-US96-07010-10	Sequence 10, Appli
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16	21	100.0	4	7	US-08-391-674-17	Sequence 17, Appli
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19	21	100.0	4	11	US-08-768-448-3	Sequence 3, Appli
20	21	100.0	4	11	US-08-768-448-5	Sequence 5, Appli
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25	21	100.0	4	13	US-08-902-766-4	Sequence 4, Appli
26	21	100.0	4	13	US-08-902-766-5	Sequence 5, Appli
27	21	100.0	4	13	US-08-902-766-10	Sequence 10, Appli
28	21	100.0	4	13	US-08-918-674-3	Sequence 3, Appli
29	21	100.0	4	13	US-08-948-124-2	Sequence 2, Appli
30	21	100.0	4	14	US-09-023-130-10	Sequence 10, Appli
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32	21	100.0	4	14	US-09-083-663-16	Sequence 16, Appli
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35	21	100.0	4	14	US-09-099-463-28	Sequence 28, Appli
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37	21	100.0	4	14	US-09-099-463A-28	Sequence 28, Appli
38	21	100.0	4	15	US-09-150-623-7	Sequence 7, Appli
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40	21	100.0	4	16	US-09-270-983-7	Sequence 7, Appli
41	21	100.0	4	16	US-09-296-662B-26	Sequence 26, Appli
42	21	100.0	4	16	US-09-296-662B-26	Sequence 26, Appli
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44	21	100.0	4	17	US-09-380-546-13	Sequence 13, Appli
45	21	100.0	4	17	US-09-380-546A-11	Sequence 11, Appli

## ALIGNMENTS

RESULT 1  
PCT-US00-09319-2  
Sequence 2, Application PC/TUS0009319  
GENERAL INFORMATION:  
APPLICANT: Cytovia, Inc.  
APPLICANT: Cai, Sui Xiong  
APPLICANT: Weber, Eckard  
APPLICANT: Wang, Yan  
APPLICANT: Mills, Gordon B.  
APPLICANT: Green, Douglas R.  
TITLE OF INVENTION: Caspase Inhibitors and the Use Thereof  
FILE REFERENCE: 1735 035PC02  
CURRENT APPLICATION NUMBER: PCT/US00/09319  
CURRENT FILING DATE: 2000-04-07  
EARLIER APPLICATION NUMBER: US 60/128,545  
EARLIER FILING DATE: 1999-04-09  
EARLIER APPLICATION NUMBER: US 60/158,370  
EARLIER FILING DATE: 1999-10-12  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 4  
TYPE: PRT

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; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: caspase-1
; OTHER INFORMATION: inhibitor
PCT-US00-09319-2

Query Match      100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YVAD 4
Db      1 YVAD 4

RESULT 2
PCT-US01-04137-2
; Sequence 2, Application PC/TUS0104137
; GENERAL INFORMATION:
; APPLICANT: ALEXION PHARMACEUTICALS, INC.
; APPLICANT: Fodor, William L.
; TITLE OF INVENTION: MIXTURES OF CASPASE INHIBITORS AND COMPLEMENT
; TITLE OF INVENTION: INHIBITORS AND METHODS OF USE THEREOF
; FILE REFERENCE: 1087-15PCT
; CURRENT APPLICATION NUMBER: PCT/US01/04137
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Caspase
; OTHER INFORMATION: inhibitor
PCT-US01-04137-2

Query Match      100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YVAD 4
Db      1 YVAD 4

RESULT 3
PCT-US01-04137-3
; Sequence 3, Application PC/TUS0104137
; GENERAL INFORMATION:
; APPLICANT: ALEXION PHARMACEUTICALS, INC.
; APPLICANT: Fodor, William L.
; TITLE OF INVENTION: MIXTURES OF CASPASE INHIBITORS AND COMPLEMENT
; TITLE OF INVENTION: INHIBITORS AND METHODS OF USE THEREOF
; FILE REFERENCE: 1087-15PCT
; CURRENT APPLICATION NUMBER: PCT/US01/04137
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Caspase
; OTHER INFORMATION: inhibitor
PCT-US01-04137-3

Query Match      100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YVAD 4
Db      1 YVAD 4

; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: caspase-1
; OTHER INFORMATION: inhibitor
PCT-US00-09319-2

Query Match      100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YVAD 4
Db      1 YVAD 4

RESULT 4
PCT-US02-18014-9
; Sequence 9, Application PC/TUS0218014
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Rechsteiner, Martin
; APPLICANT: Pratt, Gregory
; APPLICANT: Li, Jun
; TITLE OF INVENTION: METHODS FOR IDENTIFYING COMPOUNDS WITH
; TITLE OF INVENTION: THERAPEUTIC POTENTIAL FOR TREATMENT OF CENTRAL
; TITLE OF INVENTION: NEURODEGENERATIVE DISEASES RESULTING FROM ABNORMAL PROTEIN
; TITLE OF INVENTION: OR PEPTIDE ACCUMULATION
; FILE REFERENCE: 21101.0013P1
; CURRENT APPLICATION NUMBER: PCT/US02/18014
; CURRENT FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/297,332
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: /note =
; OTHER INFORMATION: synthetic construct
PCT-US02-18014-9

Query Match      100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YVAD 4
Db      1 YVAD 4

RESULT 5
PCT-US02-18484-9
; Sequence 9, Application PC/TUS0218484
; GENERAL INFORMATION:
; APPLICANT: Mitokor
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: ORGANELLAR PROTEOMES INCLUDING
; TITLE OF INVENTION: DETERMINATION OF TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME USING MASS
; TITLE OF INVENTION: SPECTROMETRY
; FILE REFERENCE: 660088.450PC
; CURRENT APPLICATION NUMBER: PCT/US02/18484
; CURRENT FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)...(1)
; OTHER INFORMATION: Benzoyl carbonyl moiety
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (4)...(4)
; OTHER INFORMATION: 7-amino-4-trifluoromethylcoumarin
PCT-US02-18484-9
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Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
Db 1 YVAD 4

RESULT 6  
PCT-US02-37577-3  
; Sequence 3, Application PC/TUS0237577  
; GENERAL INFORMATION:  
; APPLICANT: The Burnham Institute  
; APPLICANT: Reed, John C.  
; APPLICANT: Houghten, Richard A.  
; APPLICANT: Nefzi, Adel  
; APPLICANT: Ostresh, John M.  
; APPLICANT: Pinilla, Clemencia  
; APPLICANT: Welsh, Kate  
; TITLE OF INVENTION: Methode and Compositions for  
; TITLE OF INVENTION: Derepression of IAP-Inhibited Caspase  
; FILE REFERENCE: PP-LJ 5449  
; CURRENT APPLICATION NUMBER: PCT/US02/37577  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR FILING DATE: 2001-11-21  
; PRIOR FILING DATE: 2001-11-21  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic construct  
PCT-US02-37577-3

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
Db 1 YVAD 4

RESULT 7  
PCT-US03-20997-7  
; Sequence 7, Application PC/TUS0320997  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Wade, EDRIS  
; TITLE OF INVENTION: CASPASE 9 ACTIVATION AND USES THEREFOR  
; FILE REFERENCE: AM101006 PCT  
; CURRENT APPLICATION NUMBER: PCT/US03/20997  
; CURRENT FILING DATE: 2003-07-08  
; PRIOR FILING DATE: 2002-07-08  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Substrate  
PCT-US03-20997-7

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
Db 1 YVAD 4

RESULT 8  
PCT-US96-07010-10  
; Sequence 10, Application PC/TUS9607010  
; GENERAL INFORMATION:  
; APPLICANT: Litwack, Gerald  
; APPLICANT: Alnemri, Emad S.  
; APPLICANT: Fernandez-Alnemri, Teresa  
; TITLE OF INVENTION: Mch2, AN APOPTOTIC CYSTEINE  
; TITLE OF INVENTION: PROTEASE, AND COMPOSITIONS FOR  
; TITLE OF INVENTION: MAKING AND METHODS OF USING THE  
; TITLE OF INVENTION: SAME  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &  
; ADDRESSEE: Norris  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/07010  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/446,925  
; FILING DATE: 18-MAY-1995  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Deluca, Mark  
; REGISTRATION NUMBER: 33,229  
; REFERENCE/DOCKET NUMBER: TJU-1882  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-3100  
; TELEFAX: (215) 568-3439  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US96-07010-10

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
Db 1 YVAD 4

RESULT 9  
PCT-US98-12716-26  
; Sequence 26, Application PC/TUS9812716  
; GENERAL INFORMATION:  
; APPLICANT: Yuan, Junying  
; APPLICANT: Friedlander, Robert M.  
; TITLE OF INVENTION: Interleukin Converting Enzyme (ICE)  
; TITLE OF INVENTION: and Central Nervous System Damage  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

```

; STREET: 1100 New York Avenue NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/12716
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/050,242
; FILING DATE: 19-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Jorge A. Goldstein
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0609.442PC01/JAG/LBB
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /label= Ac
; OTHER INFORMATION: /note= "An acetyl (Ac) group is attached to the N-terminal"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /label= CHO
; OTHER INFORMATION: /note= "An aldehyde (CHO) is attached to the C-terminal"
; OTHER INFORMATION: aspartic acid residue."
; PCT-US98-12716-28
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; Query Match 100.0%; Score 21; DB 1; Length 4;
; Best Local Similarity 100.0%; Pred. No. 5.5e+06;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Qy 1 YVAD 4
; Db 1 YVAD 4
;
; RESULT 11
; PCT-US98-21231-2
; Sequence 2, Application PC/TUS9821231
; GENERAL INFORMATION:
; APPLICANT: Cytovia, Inc.
; TITLE OF INVENTION: Novel Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.029PC02
; CURRENT APPLICATION NUMBER: PCT/US98/21231
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,592
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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OTHER INFORMATION: Peptide  
PCT-US98-21231-2

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
Db 1 YVAD 4

## RESULT 12

PCT-US99-08064-36  
Sequence 36, Application PC/TUS9908064A

GENERAL INFORMATION:

APPLICANT: Yuan, Junying  
APPLICANT: Morishima, Nobuhiro  
APPLICANT: The General Hospital Corporation  
TITLE OF INVENTION: Programmed Cell Death and Caspase-12  
FILE REFERENCE: 0609.440PC01  
CURRENT APPLICATION NUMBER: PCT/US99/08064A  
CURRENT FILING DATE: 1999-04-14  
EARLIER APPLICATION NUMBER: US 60/081,962  
EARLIER FILING DATE: 1998-04-16  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 36

LENGTH: 4  
TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Peptide

OTHER INFORMATION: Inhibitor

PCT-US99-08064-36

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
Db 1 YVAD 4

## RESULT 13

PCT-US99-16423-2

Sequence 2, Application PC/TUS9916423

GENERAL INFORMATION:

APPLICANT: Cytovia, Inc.

APPLICANT: Zhang, Han-Zhong

APPLICANT: Cai, Sui Xiong

APPLICANT: Drewe, John A.

APPLICANT: Yang, Wu

TITLE OF INVENTION: Novel Fluorescence Dyes and Their Applications for Whole-Cell

TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Proteases

TITLE OF INVENTION: Other Enzymes and the Use Thereof

FILE REFERENCE: 1735.003PC01

CURRENT APPLICATION NUMBER: PCT/US99/16423

CURRENT FILING DATE: 1999-07-21

EARLIER APPLICATION NUMBER: US 60/093,642

EARLIER FILING DATE: 21-JUL-1998

NUMBER OF SEQ ID NOS: 139

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 4

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Peptide

PCT-US99-16423-2

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
Db 1 YVAD 4

## RESULT 14

US-08-183-269-1

Sequence 1, Application US/08183269

GENERAL INFORMATION:

APPLICANT: Molineaux, Susan M.

APPLICANT: Rolando, Anna M.

APPLICANT: Casaro, Francesca J.

TITLE OF INVENTION: DNA Encoding Murine Precursor

TITLE OF INVENTION: Interleukin 1 Beta Converting Enzyme

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merck & Co., Inc.

STREET: P.O. Box 2000

CITY: Rahway

STATE: NJ

COUNTRY: USA

ZIP: 07065

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/183,269

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/947,330

FILING DATE: 18-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Wallen, John W.

REGISTRATION NUMBER: 35,403

REFERENCE/DOCKET NUMBER: 18857

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 594-3905

TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-183-269-1

Query Match 100.0%; Score 21; DB 5; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
Db 1 YVAD 4

## RESULT 15

US-08-282-211A-16

Sequence 16, Application US/08282211A

GENERAL INFORMATION:

APPLICANT: Horvitz, H. Robert

APPLICANT: Yuan, Junying

APPLICANT: Shaham, Shai

TITLE OF INVENTION: RELATEDNESS OF HUMAN INTERLEUKIN-1

TITLE OF INVENTION: CONVERSION GENE TO A C. ELEGANS CELL DEATH GENE,

TITLE OF INVENTION: INHIBITORY PORTIONS OF THESE GENES AND USES THEREFOR

NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/282,211A  
FILING DATE: 11-JUL-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 01997/198004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-282-211A-16

Query Match 100.0%; Score 21; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. NO. 5.5e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YVAD 4  
Db 1 YVAD 4

Search completed: May 24, 2004, 14:47:41  
Job time : 176 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 24, 2004, 14:39:07 ; Search time 13.5 Seconds  
(without alignments)  
10.992 Million cell updates/sec

Title: US-09-765-105A-1

Perfect score: 21

Sequence: 1 YVAD 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 251736 seqs, 37097828 residues

Total number of hits satisfying chosen parameters: 251736

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep.\*  
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7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep.\*

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#### SUMMARIES

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2	21	100.0	4	6	US-10-627-556-528
3	21	100.0	4	6	US-10-630-926-15
4	21	100.0	4	6	US-10-829-381-2
5	21	100.0	4	6	US-10-665-668A-7
6	21	100.0	5	6	US-10-823-381-72
7	21	100.0	5	6	US-10-663-668A-6
8	21	100.0	6	6	US-10-829-381-142
9	21	100.0	14	5	US-09-394-019B-42
10	21	100.0	14	5	US-09-394-019B-43
11	21	100.0	14	5	US-09-394-019B-287
12	21	100.0	14	5	US-09-394-019B-288
13	21	100.0	14	5	US-09-394-019B-42
14	21	100.0	14	5	US-09-394-019B-43
15	21	100.0	14	5	US-09-394-019C-42
16	21	100.0	14	5	US-09-394-019C-43
17	21	100.0	14	5	US-09-394-019C-287
18	21	100.0	14	5	US-09-394-019C-288
19	21	100.0	16	5	US-09-394-019B-45
20	21	100.0	16	5	US-09-394-019B-46
21	21	100.0	16	5	US-09-394-019B-290
22	21	100.0	16	5	US-09-394-019B-291
23	21	100.0	16	5	US-09-394-019B-45
24	21	100.0	16	5	US-09-394-019B-46
25	21	100.0	16	5	US-09-394-019C-45
26	21	100.0	16	5	US-09-394-019C-46

27 21 100.0 16 5 US-09-394-019C-290 Sequence 290, App  
28 21 100.0 16 5 US-09-394-019C-291 Sequence 291, App  
29 21 100.0 18 5 US-09-394-019B-48 Sequence 48, Appl  
30 21 100.0 18 5 US-09-394-019B-51 Sequence 51, Appl  
31 21 100.0 18 5 US-09-394-019B-52 Sequence 52, Appl  
32 21 100.0 18 5 US-09-394-019B-293 Sequence 293, App  
33 21 100.0 18 5 US-09-394-019B-296 Sequence 296, App  
34 21 100.0 18 5 US-09-394-019B-297 Sequence 297, App  
35 21 100.0 18 5 US-09-394-019B-48 Sequence 48, Appl  
36 21 100.0 18 5 US-09-394-019B-51 Sequence 51, Appl  
37 21 100.0 18 5 US-09-394-019B-52 Sequence 52, Appl  
38 21 100.0 18 5 US-09-394-019C-48 Sequence 48, Appl  
39 21 100.0 18 5 US-09-394-019C-51 Sequence 51, Appl  
40 21 100.0 18 5 US-09-394-019C-52 Sequence 52, Appl  
41 21 100.0 18 5 US-09-394-019C-293 Sequence 293, App  
42 21 100.0 18 5 US-09-394-019C-296 Sequence 296, App  
43 21 100.0 18 5 US-09-394-019C-297 Sequence 297, App  
44 21 100.0 41 6 US-10-100-683-8636 Sequence 8636, Ap  
45 21 100.0 65 6 US-10-417-884A-6345 Sequence 6345, Ap

#### ALIGNMENTS

RESULT 1  
PCT-US03-41600-528  
; Sequence 528, Application PC/TUS0341600  
; GENERAL INFORMATION:  
; APPLICANT: TRIBION PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: BINDING CONSTRUCTS AND METHODS FOR USE THEREOF  
; FILE REFERENCE: 49076.000004.CIP3PCT  
; CURRENT APPLICATION NUMBER: PCT/US03/41600  
; CURRENT FILING DATE: 2003-12-24  
; PRIOR APPLICATION NUMBER: 10/627,556  
; PRIOR FILING DATE: 2003-07-26  
; NUMBER OF SEQ ID NOS: 699  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 528  
; LENGTH: 4  
; TYPE: PPT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
PCT-US03-41600-528

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4

Db 1 YVAD 4

RESULT 2  
US-10-627-556-528  
; Sequence 528, Application US/10627556  
; GENERAL INFORMATION:  
; APPLICANT: LEDBETTER, JEFFREY A.  
; APPLICANT: HAYDEN-LEDBETTER, MARTHA  
; APPLICANT: THOMPSON, PETER A.  
; TITLE OF INVENTION: BINDING CONSTRUCTS AND METHODS FOR USE THEREOF  
; FILE REFERENCE: 49076.000004.CIP2  
; CURRENT APPLICATION NUMBER: US/10/627,556  
; CURRENT FILING DATE: 2003-07-26  
; PRIOR APPLICATION NUMBER: 10/053,530  
; PRIOR FILING DATE: 2002-01-17  
; PRIOR APPLICATION NUMBER: 60/367,358  
; PRIOR FILING DATE: 2002-01-16  
; PRIOR APPLICATION NUMBER: 09/765,208  
; PRIOR FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: 60/385,691



; PRIOR FILING DATE: 2002-06-03  
; NUMBER OF SEQ ID NOS: 699  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 528  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-627-556-528

Query Match 100.0%; Score 21; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
|||  
Db 1 YVAD 4

RESULT 3  
US-10-630-926-15  
; Sequence 15, Application US/10630926  
; GENERAL INFORMATION:  
; APPLICANT: RICCARDI, Carlo  
; TITLE OF INVENTION: INTRACELLULAR MODULATORS OF APOPTIC CELL  
; DEATH PATHWAYS  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 624 Ninth Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/630,926  
; FILING DATE: 31-Jul-2003  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/403,861A  
; FILING DATE: 11-Feb-2000  
; APPLICATION NUMBER: PCT/EP98/02490  
; FILING DATE: 27-Apr-1998  
; APPLICATION NUMBER: EP 97107033.9  
; FILING DATE: 28-Apr-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YUN, Allen C.  
; REGISTRATION NUMBER: 37,971  
; REFERENCE/DOCKET NUMBER: RICCARDI=1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; OTHER INFORMATION: /note= "the N-terminus is modified by an  
; acetyl group; the C-terminus is modified with CH2OC(O)-[2,6-(CF3)2]Ph"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-10-630-926-15

Query Match 100.0%; Score 21; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
|||  
Db 1 YVAD 4

RESULT 4  
US-10-829-381-2  
; Sequence 2, Application US/10829381  
; GENERAL INFORMATION:  
; APPLICANT: Weber, Eckard  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Keana, John F.W.  
; APPLICANT: Drewe, John A.  
; APPLICANT: Zhang, Han-Zhong  
; TITLE OF INVENTION: Novel Fluorogenic or Fluorescent Reporter Molecules and  
; their Applications for Whole-Cell Fluorescence  
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the  
; TITLE OF INVENTION: Use Thereof  
; FILE REFERENCE: 1735.0290006  
; CURRENT APPLICATION NUMBER: US/10/829,381  
; CURRENT FILING DATE: 2004-04-22  
; PRIOR APPLICATION NUMBER: US 60/061,582  
; PRIOR FILING DATE: 1997-10-10  
; PRIOR APPLICATION NUMBER: US 60/145,746  
; PRIOR FILING DATE: 1998-03-03  
; PRIOR APPLICATION NUMBER: US 09/168,888  
; PRIOR FILING DATE: 1998-10-09  
; PRIOR APPLICATION NUMBER: US 09/947,387  
; PRIOR FILING DATE: 2001-09-07  
; NUMBER OF SEQ ID NOS: 142  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-10-829-381-2

Query Match 100.0%; Score 21; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
|||  
Db 1 YVAD 4

RESULT 5  
US-10-665-668A-7  
; Sequence 7, Application US/10665668A  
; GENERAL INFORMATION:  
; APPLICANT: TROY, CAROL M.  
; TITLE OF INVENTION: COMPOUNDS WHICH PREVENT CELL DEATH AND USES THEREOF  
; FILE REFERENCE: 0575/48332-B  
; CURRENT APPLICATION NUMBER: US/10/665,668A  
; CURRENT FILING DATE: 2003-09-19  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: MOTIF OF PSEUDOSUBSTRATE INHIBITOR  
US-10-665-668A-7

Query Match 100.0%; Score 21; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
| | | |  
Db 1 YVAD 4

RESULT 6  
US-10-829-381-72  
; Sequence 72, Application US/10829381  
; GENERAL INFORMATION:  
; APPLICANT: Weber, Eckard  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Keana, John F.W.  
; APPLICANT: Drewe, John A.  
; APPLICANT: Zhang, Han-Zhong  
; TITLE OF INVENTION: Novel Fluorogenic or Fluorescent Reporter Molecules and  
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence  
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the  
; TITLE OF INVENTION: Use Thereof  
; FILE REFERENCE: 1735.0290006  
; CURRENT APPLICATION NUMBER: US/10/829,381  
; CURRENT FILING DATE: 2004-04-22  
; PRIOR APPLICATION NUMBER: US 60/061,582  
; PRIOR FILING DATE: 1997-10-10  
; PRIOR APPLICATION NUMBER: US 60/145,746  
; PRIOR FILING DATE: 1998-03-03  
; PRIOR APPLICATION NUMBER: US 09/168,888  
; PRIOR FILING DATE: 1998-10-09  
; PRIOR APPLICATION NUMBER: US 09/947,387  
; PRIOR FILING DATE: 2001-09-07  
; NUMBER OF SEQ ID NOS: 142  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 72  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-10-829-381-72

Query Match 100.0%; Score 21; DB 6; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
| | | |  
Db 1 YVAD 4

RESULT 7  
US-10-665-668A-6  
; Sequence 6, Application US/10665668A  
; GENERAL INFORMATION:  
; APPLICANT: TROY, CAROL M.  
; TITLE OF INVENTION: COMPOUNDS WHICH PREVENT CELL DEATH AND USES THEREOF  
; FILE REFERENCE: 0575/48332-B  
; CURRENT APPLICATION NUMBER: US/10/665,668A  
; CURRENT FILING DATE: 2003-09-19  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: COMPETITIVE INHIBITOR OF ICE  
US-10-665-668A-6

Query Match 100.0%; Score 21; DB 6; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4

Db 2 YVAD 5  
| | | |

RESULT 8  
US-10-829-381-142  
; Sequence 142, Application US/10829381  
; GENERAL INFORMATION:  
; APPLICANT: Weber, Eckard  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Keana, John F.W.  
; APPLICANT: Drewe, John A.  
; APPLICANT: Zhang, Han-Zhong  
; TITLE OF INVENTION: Novel Fluorogenic or Fluorescent Reporter Molecules and  
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence  
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the  
; TITLE OF INVENTION: Use Thereof  
; FILE REFERENCE: 1735.0290006  
; CURRENT APPLICATION NUMBER: US/10/829,381  
; CURRENT FILING DATE: 2004-04-22  
; PRIOR APPLICATION NUMBER: US 60/061,582  
; PRIOR FILING DATE: 1997-10-10  
; PRIOR APPLICATION NUMBER: US 60/145,746  
; PRIOR FILING DATE: 1998-03-03  
; PRIOR APPLICATION NUMBER: US 09/168,888  
; PRIOR FILING DATE: 1998-10-09  
; PRIOR APPLICATION NUMBER: US 09/947,387  
; PRIOR FILING DATE: 2001-09-07  
; NUMBER OF SEQ ID NOS: 142  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 142  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-10-829-381-142

Query Match 100.0%; Score 21; DB 6; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
| | | |  
Db 1 YVAD 4

RESULT 9  
US-09-394-019B-42  
; Sequence 42, Application US/09394019B  
; GENERAL INFORMATION:  
; APPLICANT: Oncoimmun, Inc.  
; APPLICANT: Komoriya, Akira  
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL  
; FILE REFERENCE: 300-903820US  
; CURRENT APPLICATION NUMBER: US/09/394,019B  
; CURRENT FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: PCT/US98/00300  
; PRIOR FILING DATE: 1998-02-20  
; PRIOR APPLICATION NUMBER: US 08/802,981  
; PRIOR FILING DATE: 1997-02-20  
; NUMBER OF SEQ ID NOS: 405  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 42  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide substrate  
; FEATURE:

```
; NAME/KEY: MOD_RES
; LOCATION: (3)..(3)
; OTHER INFORMATION: X is Alb
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-394-019B-42

Query Match      100.0%; Score 21; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YVAD 4
        ||||
Db      4 YVAD 7

RESULT 10
US-09-394-019B-43
; Sequence 43, Application US/09394019B
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
; FILE REFERENCE: 300-903820US
; CURRENT APPLICATION NUMBER: US/09/394,019B
; CURRENT FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 43
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide substrate
; NAME/KEY: MOD_RES
; LOCATION: (3)..(3)
; OTHER INFORMATION: X is Alb
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-394-019B-43

Query Match      100.0%; Score 21; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YVAD 4
        ||||
Db      4 YVAD 7

RESULT 11
US-09-394-019B-287
; Sequence 287, Application US/09394019B
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
; FILE REFERENCE: 300-903820US
; CURRENT APPLICATION NUMBER: US/09/394,019B
; CURRENT FILING DATE: 1999-09-10
```

```
; NAME/KEY: MOD_RES
; LOCATION: (3)..(3)
; OTHER INFORMATION: X is Alb
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-394-019B-42

Query Match      100.0%; Score 21; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YVAD 4
        ||||
Db      4 YVAD 7

RESULT 10
US-09-394-019B-43
; Sequence 43, Application US/09394019B
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
; FILE REFERENCE: 300-903820US
; CURRENT APPLICATION NUMBER: US/09/394,019B
; CURRENT FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 43
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide substrate
; NAME/KEY: MOD_RES
; LOCATION: (3)..(3)
; OTHER INFORMATION: X is Alb
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-394-019B-43

Query Match      100.0%; Score 21; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YVAD 4
        ||||
Db      4 YVAD 7

RESULT 11
US-09-394-019B-287
; Sequence 287, Application US/09394019B
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
; FILE REFERENCE: 300-903820US
; CURRENT APPLICATION NUMBER: US/09/394,019B
; CURRENT FILING DATE: 1999-09-10
```

```
; NAME/KEY: MOD_RES
; LOCATION: (3)..(3)
; OTHER INFORMATION: X is Alb
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-394-019B-42

Query Match      100.0%; Score 21; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YVAD 4
        ||||
Db      4 YVAD 7

RESULT 10
US-09-394-019B-43
; Sequence 43, Application US/09394019B
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
; FILE REFERENCE: 300-903820US
; CURRENT APPLICATION NUMBER: US/09/394,019B
; CURRENT FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 43
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide substrate
; NAME/KEY: MOD_RES
; LOCATION: (3)..(3)
; OTHER INFORMATION: X is Alb
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-394-019B-43

Query Match      100.0%; Score 21; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YVAD 4
        ||||
Db      4 YVAD 7

RESULT 11
US-09-394-019B-287
; Sequence 287, Application US/09394019B
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
; FILE REFERENCE: 300-903820US
; CURRENT APPLICATION NUMBER: US/09/394,019B
; CURRENT FILING DATE: 1999-09-10
```

```
; NAME/KEY: MOD_RES
; LOCATION: (3)..(3)
; OTHER INFORMATION: X is Alb
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa is alpha-aminoisobutyric acid
US-09-394-019B-287

Query Match      100.0%; Score 21; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YVAD 4
        ||||
Db      4 YVAD 7

RESULT 12
US-09-394-019B-288
; Sequence 288, Application US/09394019B
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
; FILE REFERENCE: 300-903820US
; CURRENT APPLICATION NUMBER: US/09/394,019B
; CURRENT FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 288
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide. Chemically synthesized protease substrate.
; NAME/KEY: misc feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa is alpha-aminoisobutyric acid
US-09-394-019B-288

Query Match      100.0%; Score 21; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YVAD 4
        ||||
Db      4 YVAD 7

RESULT 13
US-09-394-019B-42
; Sequence 42, Application US/09394019B
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
; FILE REFERENCE: 300-903820US
; CURRENT APPLICATION NUMBER: US/09/394,019B
; CURRENT FILING DATE: 1999-09-10
```

/ TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL  
/ TITLE OF INVENTION: AND METHODS OF USE THEREOF  
/ FILE REFERENCE: M-903820US  
/ CURRENT APPLICATION NUMBER: US/09/394,019B  
/ CURRENT FILING DATE: 1999-09-10  
/ PRIOR APPLICATION NUMBER: PCT/US98/00300  
/ PRIOR FILING DATE: 1998-02-20  
/ PRIOR APPLICATION NUMBER: US 08/802,981  
/ PRIOR FILING DATE: 1997-02-20  
/ NUMBER OF SEQ ID NOS: 257  
/ SOFTWARE: PatentIn version 3.0  
/ SEQ ID NO 42  
/ LENGTH: 14  
/ TYPE: PRT  
/ ORGANISM: Artificial  
/ FEATURE:  
/ FEATURE: Synthetic peptide substrate  
/ NAME/KEY: MOD\_RES  
/ LOCATION: (3)..(3)  
/ OTHER INFORMATION: Xaa is Aib  
/ US-09-394-019B-42

Query Match 100.0%; Score 21; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
|||  
Db 4 YVAD 7

RESULT 14  
US-09-394-019B-43  
/ Sequence 43, Application US/09394019B  
/ GENERAL INFORMATION:  
/ APPLICANT: Oncoimmunin, Inc.  
/ APPLICANT: Komoriya, Akira  
/ TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL  
/ TITLE OF INVENTION: AND METHODS OF USE THEREOF  
/ FILE REFERENCE: M-903820US  
/ CURRENT APPLICATION NUMBER: US/09/394,019B  
/ CURRENT FILING DATE: 1999-09-10  
/ PRIOR APPLICATION NUMBER: PCT/US98/00300  
/ PRIOR FILING DATE: 1998-02-20  
/ PRIOR APPLICATION NUMBER: US 08/802,981  
/ PRIOR FILING DATE: 1997-02-20  
/ NUMBER OF SEQ ID NOS: 257  
/ SOFTWARE: PatentIn version 3.0  
/ SEQ ID NO 43  
/ LENGTH: 14  
/ TYPE: PRT  
/ ORGANISM: Artificial  
/ FEATURE:  
/ FEATURE: Synthetic peptide substrate  
/ NAME/KEY: MOD\_RES  
/ LOCATION: (3)..(3)  
/ OTHER INFORMATION: Xaa is Aib  
/ US-09-394-019B-43

Query Match 100.0%; Score 21; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
|||  
Db 4 YVAD 7

RESULT 15  
US-09-394-019C-42

/ Sequence 42, Application US/09394019C  
/ GENERAL INFORMATION:  
/ APPLICANT: Oncoimmunin, Inc.  
/ APPLICANT: Komoriya, Akira  
/ TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL  
/ TITLE OF INVENTION: SAMPLES AND METHODS OF USE THEREOF  
/ FILE REFERENCE: 300-903820US  
/ CURRENT APPLICATION NUMBER: US/09/394,019C  
/ CURRENT FILING DATE: 1999-09-10  
/ PRIOR APPLICATION NUMBER: PCT/US98/00300  
/ PRIOR FILING DATE: 1998-02-20  
/ PRIOR APPLICATION NUMBER: US 08/802,981  
/ PRIOR FILING DATE: 1997-02-20  
/ NUMBER OF SEQ ID NOS: 405  
/ SOFTWARE: PatentIn version 3.2  
/ SEQ ID NO 42  
/ LENGTH: 14  
/ TYPE: PRT  
/ ORGANISM: Artificial  
/ FEATURE:  
/ FEATURE: Synthetic peptide substrate  
/ NAME/KEY: MOD\_RES  
/ LOCATION: (3)..(3)  
/ OTHER INFORMATION: X is Aib  
/ FEATURE:  
/ NAME/KEY: misc\_feature  
/ LOCATION: (3)..(3)  
/ OTHER INFORMATION: Xaa can be any naturally occurring amino acid  
/ US-09-394-019C-42

Query Match 100.0%; Score 21; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
|||  
Db 4 YVAD 7

Search completed: May 24, 2004, 14:48:20  
Job time : 13.5 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 24, 2004, 14:36:18 ; Search time 13.5 Seconds  
(without alignments)  
28.501 Million cell updates/sec

Title: US-09-765-105A-1

Perfect score: 21

Sequence: 1 YVAD 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:\*

1: P1r1:\*

2: P1r2:\*

3: P1r3:\*

4: P1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	32	2 S20719	alcohol dehydrogen
2	21	100.0	43	2 A24553	cuticle protein SC
3	21	100.0	54	2 H82718	hypothetical prote
4	21	100.0	66	2 PC4222	GTP-binding protei
5	21	100.0	66	2 PC4266	GTP-binding protei
6	21	100.0	68	2 G82969	probable transcrip
7	21	100.0	75	2 AC1251	hypothetical prote
8	21	100.0	76	2 S51629	FRAC-6 protein -
9	21	100.0	77	1 R3BS18	ribosomal protein
10	21	100.0	80	2 AG1613	hypothetical prote
11	21	100.0	82	2 IS1103	Major Histocompati
12	21	100.0	82	2 IS1106	Major Histocompati
13	21	100.0	82	2 E71321	hypothetical prote
14	21	100.0	86	2 A28093	GTP-binding protei
15	21	100.0	88	2 S71291	retrovirus-related
16	21	100.0	88	2 H87560	conserved hypotet
17	21	100.0	94	2 G69597	conserved hypotet
18	21	100.0	94	2 AB2197	hypothetical prote
19	21	100.0	95	2 A43027	T-cell receptor va
20	21	100.0	95	2 H42409	glutathione transf
21	21	100.0	97	2 AD2153	hypothetical prote
22	21	100.0	97	2 F97952	phospho-beta-gluc
23	21	100.0	98	2 A87437	hypothetical prote
24	21	100.0	101	2 A47450	HNF-3/foxa-head ho
25	21	100.0	102	2 T29100	hypothetical prote
26	21	100.0	102	2 B89860	conserved hypotet
27	21	100.0	106	2 D90247	conserved hypotet
28	21	100.0	112	2 C23766	modulation protein
29	21	100.0	113	2 D27664	T-cell receptor be

30 21 100.0 113 2 D64593 ferredoxin-like pr  
31 21 100.0 113 2 F71919 chain of 2-oxogluc  
32 21 100.0 113 2 D70757 probable regulator  
33 21 100.0 114 2 G84409 hypothetical prote  
34 21 100.0 115 2 H86734 HU-like DNA-bindin  
35 21 100.0 119 2 D95146 conserved hypotet  
36 21 100.0 119 2 C98014 conserved hypotet  
37 21 100.0 120 2 AF0108 probable DNA bindi  
38 21 100.0 120 2 ABC490 probable regulator  
39 21 100.0 122 1 RWMSC5 T-cell receptor be  
40 21 100.0 122 2 F84287 hypothetical prote  
41 21 100.0 123 2 T49794 hypothetical prote  
42 21 100.0 125 2 S01374 cuticle protein LC  
43 21 100.0 129 2 S78097 endocuticular prot  
44 21 100.0 131 2 AE1355 hypothetical prote  
45 21 100.0 131 2 A99502 conserved hypotet

#### ALIGNMENTS

##### RESULT 1

S20719

alcohol dehydrogenase related protein (EC 1.1.1.1.-) - fruit fly (*Drosophila yakuba*) (fr  
N/Alternate names: Adh-dup protein; Adh-related protein; Adhr protein; alcohol dehydro  
C:Species: *Drosophila yakuba*

C>Date: 20-Feb-1995 #sequence\_revision 19-Apr-1996 #text\_change 11-Jun-1999

C/Accession: S20719

R.Ashburner, M.

submitted to the EMBL Data Library, July 1990

A/Reference number: S20713

A/Accession: S20719

A/Molecule type: DNA

A/Residues: 1-32 <ASH>

A/Cross-references: EMBL:X54120; NID:g9214; PIDN:CAA38064.1; PID:g9216

C/Genetics:

A/Gens: FlyBase:Adhr; Adh-dup

A/Cross-references: FlyBase:FBgn0013164

C/Suprafamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

C/Keywords: oxidoreductase

Query Match 100.0%; Score 21; DB 2; Length 32;  
Best Local Similarity 100.0%; Pred. No. 54; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

QY 1 YVAD 4  
|||  
DB 11 YVAD 14

##### RESULT 2

A24553

cuticle protein SC1 - flesh fly (*Sarcophaga bullata*) (fragment)

C/Species: *Sarcophaga bullata*

C/Date: 29-Aug-1987 #sequence\_revision 29-Aug-1987 #text\_change 18-Jun-1993

C/Accession: A24553

R/Henzel, W.J.; Mole, J.E.; Mulligan, K.; Lipke, H.

J. Mol. Evol. 22, 39-45, 1985

A/Title: *Sarcophagid* larval proteins: partial sequence homologies among three cuticle  
A/Reference number: A32963; MUID:86037264; PMID:3932663

A/Accession: A24553

A/Molecule type: protein

A/Residues: 1-43 <HEN>

C/Suprafamily: cuticle protein LCPI

Query Match 100.0%; Score 21; DB 2; Length 43;  
Best Local Similarity 100.0%; Pred. No. 74; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

QY 1 YVAD 4  
|||  
DB 39 YVAD 42

**RESULT 3**  
 H82718  
 hypothetical protein Xfl129 [imported] - Xylella fastidiosa (strain 9a5c)  
 C/Species: Xylella fastidiosa  
 C/Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
 C/Accession: H82718  
 R/Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing  
 A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
 A/Reference number: A82515; MUID:20365717; PMID:10910347  
 A/Note: for a complete list of authors see reference number A59328 below  
 A/Accession: H82718  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-54 <SIM>  
 A/Cross-references: GB:AE003949; GB:AE003849; NID:g9106088; PIDN:AP83939.1; GSPDB:GN001  
 A/Experimental source: strain 9a5c  
 B/Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; B  
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H  
 as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.  
 submitted to GenBank, June 2000  
 A/Authors: Ferreira, V.C.A.; Ferro, J.S.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm  
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig  
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E  
 A/Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.  
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A  
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak  
 A/Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir  
 M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
 A/Reference number: A59328  
 A/Contents: annotation  
 C/Genetics:  
 A/Gene: Xfl129  
 Query Match 100.0%; Score 21; DB 2; Length 54;  
 Best Local Similarity 100.0%; Pred. No. 94;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YVAD 4  
 Db 50 YVAD 53

**RESULT 4**  
 PC4222  
 GTP-binding protein rhoA - pig (fragment)  
 C/Species: Sus scrofa domestica (domestic pig)  
 C/Date: 31-Jan-1997 #sequence\_revision 31-Jan-1997 #text\_change 20-Jun-2000  
 C/Accession: PC4222  
 R/Nishimura, J.; Sakihara, C.; Zhou, Y.; Kanaide, H.  
 Biochem. Biophys. Res. Commun. 227, 750-754, 1996  
 A/Title: Expression of rho A and rho kinase mRNAs in porcine vascular smooth muscle.  
 A/Reference number: PC4222; MUID:97040692; PMID:8886005  
 A/Accession: PC4222  
 A/Molecule type: mRNA  
 A/Residues: 1-66 <NIS>  
 A/Cross-references: DDBJ:D89492; NID:g1695730; PIDN:BAAL1966.1; PID:g1695731  
 C/Comment: This protein is involved in the inhibition of myosin light chain phosphatase.  
 C/Genetics:  
 A/Gene: rhoA  
 C/Superfamily: ras transforming protein; translation elongation factor Tu homology  
 C/Keywords: GTP binding  
 Query Match 100.0%; Score 21; DB 2; Length 66;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YVAD 4  
 Db 7 YVAD 10

**RESULT 5**  
 PC4266  
 GTP-binding protein rhoA - rat (fragment)  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 28-May-1997 #sequence\_revision 18-Jul-1997 #text\_change 13-Aug-1999  
 C/Accession: PC4266  
 R/Niito, N.; Nishimura, J.; Sakihara, C.; Nakano, H.; Kanaide, H.  
 Biochem. Biophys. Res. Commun. 230, 356-359, 1997  
 A/Title: Up-regulation of rho A and rho-kinase mRNAs in the rat myometrium during pregn  
 A/Reference number: PC4266; MUID:97169976; PMID:9016783  
 A/Accession: PC4266  
 A/Molecule type: mRNA  
 A/Residues: 1-66 <NII>  
 C/Comment: This protein is involved in the Ca2+ sensitivity of the smooth muscle myofil  
 C/Superfamily: ras transforming protein; translation elongation factor Tu homology  
 C/Keywords: GTP binding  
 Query Match 100.0%; Score 21; DB 2; Length 66;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YVAD 4  
 Db 7 YVAD 10

**RESULT 6**  
 G82969  
 probable transcription regulator PA5403 [imported] - Pseudomonas aeruginosa (strain PAO  
 C/Species: Pseudomonas aeruginosa  
 C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
 C/Accession: G82969  
 R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B  
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim  
 Lory, S.; Olson, M.V.  
 Nature 406, 959-964, 2000  
 A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path  
 A/Reference number: A82950; MUID:20437337; PMID:10984043  
 A/Accession: G82969  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-68 <STO>  
 A/Cross-references: GB:AE004953; GB:AE004091; NID:g9951727; PIDN:AG08788.1; GSPDB:GN00  
 A/Experimental source: strain PA01  
 C/Genetics:  
 A/Gene: PA5403  
 Query Match 100.0%; Score 21; DB 2; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YVAD 4  
 Db 64 YVAD 67

**RESULT 7**  
 AC1251  
 hypothetical protein lnc1411 [imported] - Listeria monocytogenes (strain EGD-e)  
 C/Species: Listeria monocytogenes  
 C/Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001  
 C/Accession: AC1251  
 R/Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke  
 ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl, H  
 D.; Jones, L.M.; Karst, U.  
 Science 294, 843-852, 2001  
 A/Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M  
 ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland  
 A/Title: Comparative genomics of Listeria species.  
 A/Reference number: AB1077; MUID:21537279; PMID:11679669  
 A/Accession: AC1251  
 A/Status: preliminary  
 A/Molecule type: DNA

A;Residues: 1-75 <GLA>  
A;Cross-references: GB:NC\_003210; PIDN:CA99489.1; PID:gl6410840; GSPDB:GN00177  
A;Experimental source: strain EGB-e  
C;Genetics:  
A;Gene: lnc1411

Query Match 100.0%; Score 21; DB 2; Length 75;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4  
Db 65 YVAD 68

RESULT 8  
S51629  
FRAC-6 protein - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 24-Sep-1999  
R;Accession: S51629  
R;Pierrou, S.; Hellqvist, M.; Samuelsson, L.; Enerbaeck, S.; Carlsson, P.  
EMBO J. 13, 5002-5012, 1994  
A;Title: Cloning and characterization of seven human forkhead proteins: binding site spe  
A;Reference number: S51624; MUID:95045392; PMID:7957066  
A;Status: preliminary; nucleic acid sequence not shown  
A;Accession: S51629  
A;Molecule type: mRNA  
A;Residues: 1-76 <PE>  
A;Cross-references: EMBL:U13224; NID:G563167; PIDN:AAA92041.1; PID:G563168  
C;Genetics:  
A;Gene: GDB:FKHL10; FRAC6  
A;Cross-references: GDB:450228; OMIM:601093  
A;Map position: 5q34-5q34  
C;Superfamily: unassigned fork head proteins; fork head DNA-binding domain homology  
P;6-76/Domain: fork head DNA-binding domain homology (fragment) <FHD>

Query Match 100.0%; Score 21; DB 2; Length 76;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4  
Db 35 YVAD 38

RESULT 9  
R3BS18  
ribosomal protein S18 - Bacillus stearothermophilus  
C;Species: Bacillus stearothermophilus  
C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 30-Jun-1993  
R;McDougall, J.; Choli, T.; Kruft, V.; Kapp, U.; Wittmann-Liebold, B.  
FEBS Lett. 245, 253-260, 1989  
A;Title: The complete amino acid sequence of ribosomal protein S18 from the moderate the  
A;Reference number: S03556; MUID:89171319; PMID:2647521  
A;Accession: S03556  
A;Molecule type: protein  
A;Residues: 1-77 <MCD>  
C;Superfamily: Escherichia coli ribosomal protein S18  
C;Keywords: protein biosynthesis; ribosome

Query Match 100.0%; Score 21; DB 1; Length 77;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4  
Db 73 YVAD 76

RESULT 10  
AG1613

hypothetical protein lin1448 [imported] - Listeria innocua (strain Clip11262)  
C;Species: Listeria innocua  
C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001  
C;Accession: AG1613  
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeck  
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl,  
D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A;Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.;  
Ok, C.; Schlueter, T.; Simoes, N.; Tiersz, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlan  
A;Title: Comparative genomics of Listeria species.  
A;Reference number: AB1077; MUID:21537279; PMID:11679669  
A;Accession: AG1613  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-80 <GLA>  
A;Cross-references: GB:AL592022; PIDN:CA996679.1; PID:gl6413921; GSPDB:GN00178  
A;Experimental source: strain Clip11262  
C;Genetics:  
A;Gene: lin1448

Query Match 100.0%; Score 21; DB 2; Length 80;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4  
Db 70 YVAD 73

RESULT 11  
IS1103  
Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)  
C;Species: Phasianus colchicus (ring-necked pheasant)  
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 23-Jul-1999  
C;Accession: IS1103  
R;Witzell, H.; von Schantz, T.; Zoorob, R.; Auftray, C.  
Immunogenetics 39, 395-403, 1994  
A;Title: Molecular characterization of three Mhc class II B haplotypes in the ring-nec  
A;Reference number: IS1103; MUID:94245280; PMID:7910588  
A;Accession: IS1103  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 1-82 <MIT>  
A;Cross-references: EMBL:X75403; NID:G496920; PIDN:CAAS3157.1; PID:G496921  
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 100.0%; Score 21; DB 2; Length 82;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4  
Db 42 YVAD 45

RESULT 12  
IS1106  
Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)  
C;Species: Phasianus colchicus (ring-necked pheasant)  
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 23-Jul-1999  
C;Accession: IS1106  
R;Witzell, H.; von Schantz, T.; Zoorob, R.; Auftray, C.  
Immunogenetics 39, 395-403, 1994  
A;Title: Molecular characterization of three Mhc class II B haplotypes in the ring-nec  
A;Reference number: IS1103; MUID:94245280; PMID:7910588  
A;Accession: IS1106  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 1-82 <MIT>  
A;Cross-references: EMBL:X75406; NID:G496926; PIDN:CAAS3160.1; PID:G496927  
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology

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Query Match      100.0%; Score 21; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
   ||||
Db 42 YVAD 45

RESULT 13
EY1321
Hypothetical protein TP0467 - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
C:Accession: EY1321
R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khaliq, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uitterback, T.; McDoe
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A>Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:9665876
A:Accession: EY1321
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-82 <COL>
A:Cross-references: GB:AE001223; GB:AE000520; NID:93322745; PIDN:AAC65458.1; PID:9332275
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0467

Query Match      100.0%; Score 21; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
   ||||
Db 31 YVAD 34

RESULT 14
A28093
GTP-binding protein rhoB - bovine (fragments)
N:Alternate names: 20K GTP-binding protein rho; rhoB* protein; transforming protein rhoB
C:Species: Bos primigenius taurus (cattle)
C>Date: 26-Jan-1989 #sequence_revision 05-Apr-1995 #text_change 13-Aug-1999
C:Accession: A28093; B38324; E60050
R:Yamamoto, K.; Kondo, J.; Hishida, T.; Teranishi, Y.; Takai, Y.
J. Biol. Chem. 263, 9926-9932, 1988
A>Title: Purification and characterization of a GTP-binding protein with a molecular wei
A:Reference number: A28093; MUID:88257127; PMID:3133371
A:Accession: A28093
A:Molecule type: protein
A:Residues: 25-47;48-53 <YAM>
A:Experimental source: brain
R:Williamson, K.C.; Smith, L.A.; Moss, J.; Vaughan, M.
J. Biol. Chem. 265, 20807-20812, 1990
A>Title: Guanine nucleotide-dependent ADP-ribosylation of soluble rho catalyzed by Clostr
A:Reference number: A38324; MUID:91065876; PMID:2174426
A:Accession: B38324
A:Molecule type: protein
A:Residues: 1-43;48-53;69-71 <WL>
A:Experimental source: brain
R:Hoshijima, M.; Kondo, J.; Kikuchi, A.; Yamamoto, K.; Takai, Y.
Brain Res. Mol. Brain Res. 7, 9-16, 1990
A>Title: Purification and characterization from bovine brain membranes of a GTP-binding
C1 - identification as the rhoA gene product.
A:Reference number: A60050; MUID:90135940; PMID:2153899
A:Accession: B60050
A:Molecule type: protein
A:Residues: 54-68;72-86 <HO2>
A:Experimental source: brain
C:Genetics:
A:Gene: rhoB
```

C:Superfamily: ras transforming protein; translation elongation factor Tu homology  
C:Keywords: GTP binding; immediate-early protein; transforming protein  
F:51-54/Region: GTP-binding NKXD motif

Query Match 100.0%; Score 21; DB 2; Length 86;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
 ||||  
Db 15 YVAD 18

RESULT 15  
S71291  
retrovirus-related reverse transcriptase homolog (clone Rcat3) - Arabidopsis thaliana (C:Species: Arabidopsis thaliana (mouse-ear cress)  
A:Variety: Strain Columbia  
C>Date: 18-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000  
C:Accession: S71291  
R:Brandes, A.; Heslop-Harrison, J.S.; Kamm, A.; Kubis, S.; Doudrick, R.L.; Schmidt, T.  
submitted to the EMBL Data Library, January 1996  
A:Description: Comparative analysis of the chromosomal and genomic organization of Ty1-  
A:Reference number: S71291  
A:Accession: S71291  
A:Molecule type: DNA  
A:Residues: 1-88 <BRA>  
A:Cross-references: EMBL:268911; NID:g1171493; PIDN:CAA93146.1; PID:g1171494  
C:Genetics:  
A:Mobile element: retrotransposon copia-like Ty1  
C:Superfamily: retrovirus-related polyprotein  
C:Keywords: reverse transcriptase

Query Match 100.0%; Score 21; DB 2; Length 88;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
 ||||  
Db 20 YVAD 23

Search completed: May 24, 2004, 14:41:39  
Job time : 14.5 secs



GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: May 24, 2004, 14:36:17 ; Search time 10.5 Seconds  
(without alignments)  
19.836 Million cell updates/sec

Title: US-09-765-105a-1

Perfect score: 21

Sequence: 1 YVAD 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	32	ADHR_DROVA	P2487 drosophila
2	21	100.0	36	PAHO_RABIT	P41336 oryctolagus
3	21	100.0	37	ATPO_SOLTU	P80504 solanum tub
4	21	100.0	43	CUP1_SARBU	P14485 sarcophaga
5	21	100.0	74	RS18_CHLTE	Q8kam3 chlorobium
6	21	100.0	75	HP18_RHOE	P80882 rhodofarax
7	21	100.0	77	RS18_BACST	P10806 bacillus st
8	21	100.0	82	Y467_TREPA	Q83480 treponema p
9	21	100.0	94	YQGV_BACSU	P54499 bacillus su
10	21	100.0	102	CPA1_CANPG	P81575 cancer pagu
11	21	100.0	104	LCPS_DROME	P32192 drosophila
12	21	100.0	105	CPA2_CANPG	P81576 cancer pagu
13	21	100.0	113	YJ50_WYCTU	Q10868 mycobacteri
14	21	100.0	117	GLRA_ACALA	P30970 acanthopagr
15	21	100.0	122	TVBS_MOUSE	P04213 mus musculu
16	21	100.0	125	CUI4_MANSE	P32229 manduca sex
17	21	100.0	126	CLP2_DROMI	P91627 drosophila
18	21	100.0	138	CLP1_DROMI	P91627 drosophila
19	21	100.0	143	CUI7_BOMMO	Q02387 bombyx mori
20	21	100.0	152	ACPM_DROME	Q84519 drosophila
21	21	100.0	156	CUS5_ARADI	P80518 araneus dia
22	21	100.0	159	CUS7_ARADI	P80519 araneus dia
23	21	100.0	159	OBP_BOVIN	P07435 bos taurus
24	21	100.0	161	HS21_MAIZE	P24631 zea mays (m
25	21	100.0	163	DTD_NSIWA	Q91st7 neisseria m
26	21	100.0	171	Y041_NPVOP	Q10301 oxygia pseu
27	21	100.0	174	AROK_STAAW	Q98tv6 staphylococ
28	21	100.0	174	AROK_STAAW	Q8awc8 staphylococ
29	21	100.0	174	CUS2_BOMMO	Q02388 bombyx mori
30	21	100.0	180	CYSH_RHIRT	Q33579 rhizobium t
31	21	100.0	182	APT_PSEPK	Q88f33 pseudomonas
32	21	100.0	182	NODC_RHILT	P04678 rhizobium l
33	21	100.0	184	CUPP_DROME	P14484 drosophila

34	21	100.0	186	1	YQEK_BACSU	P54456 bacillus su
35	21	100.0	192	1	CUPP_DROPS	P16369 drosophila
36	21	100.0	192	1	RHO1_DROME	P48148 drosophila
37	21	100.0	192	1	RHO1_CAEEL	Q22038 caenorhabdi
38	21	100.0	192	1	RHO1_APLCA	P01122 aplysia cal
39	21	100.0	192	1	RHO1_DISOM	P22122 discopys o
40	21	100.0	193	1	RHO1_CANFA	P24406 canis fami
41	21	100.0	193	1	RHO1_HUMAN	P06749 homo sapien
42	21	100.0	193	1	RHO1_MOUSE	Q9qu10 mus musculu
43	21	100.0	194	1	MOBA_ECOL6	Q8fbh7 escherichia
44	21	100.0	196	1	RHO1_HUMAN	P01121 homo sapien
45	21	100.0	198	1	RHO1_CANAL	O42825 candida alb

## ALIGNMENTS

### RESULT 1

ADHR\_DROVA  
ID ADHR\_DROVA STANDARD; PRT; 32 AA.  
AC P28487;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Alcohol dehydrogenase related 31 kDa protein (Fragment).  
GN ADHR.  
OS Drosophila yakuba (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7245;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ashburner M.;  
RL Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases  
(SDR) family.  
CC  
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CC  
CC EMBL; X54120; CAA38064.1; -.  
CC PIR; S20719; S20719.  
CC FlyBase; FBgn0013164; Dyak\Adhr.  
CC InterPro; IPR002198; ADH\_SHORT.  
CC PROSITE; PS00061; ADH\_SHORT; PARTIAL.  
KW Oxidoreductase.  
FT NP\_BIND 11 >32 NAD OR NADP (BY SIMILARITY).  
FT NON\_TER 32  
SQ SEQUENCE 32 AA; 3412 MW; 9302949AFCBE7D4F CRC64;

Query Match 100.0%; Score 21; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4

DB 11 YVAD 14

### RESULT 2

PAHO\_RABIT  
ID PAHO\_RABIT STANDARD; PRT; 36 AA.  
AC P41336;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Pancreatic hormone (Pancreatic polypeptide) (pp).

GN PPY.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pancreas;  
 RX MEDLINE=94130533; PubMed=8299350;  
 RA Marks N.J., Shaw C., Halton D.W., Curry W.J., Thim L.;  
 RT "Rabbit pancreatic polypeptide";  
 RL Comp. Biochem. Physiol. 106B:883-887(1993).  
 CC -!- FUNCTION: Pancreatic hormone is synthesized in pancreatic islets  
 CC of Langerhans and acts as a regulator of pancreatic and  
 CC gastrointestinal functions.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the NPY family.  
 DR HSSP: P01302; IBB.  
 DR InterPro: IPR001955; Pancreatic\_hormn.  
 DR Pfam: PF00159; hormones; 1.  
 DR PRINTS: PR00278; PANCHORMONE.  
 DR SMART: SM00309; PAH; 1.  
 DR PROSITE: PS00265; PANCREATIC\_HORMONE\_1; 1.  
 DR PROSITE: PS00276; PANCREATIC\_HORMONE\_2; 1.  
 KW Hormone; Amidation; Pancreas.  
 FT MOD RES 36  
 SQ SEQUENCE 36 AA; 4187 MW; AL4450831A7759D CRC64;  
 Query Match 100.0%; Score 21; DB 1; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 32;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YVAD 4  
 Db ||||  
 20 YVAD 23  
 RESULT 3  
 ID \_ATPO SOLTU STANDARD; PRT; 37 AA.  
 AC P80504; 1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DE 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE ATP synthase delta chain, mitochondrial (EC 3.6.3.14) (Oligomycin  
 DE sensitivity conferral protein) (OSCP) (Fragment).  
 OS Solum tuberosum (Potato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Lamids; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4113;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Tuber;  
 RX MEDLINE=97077345; PubMed=8919912;  
 RA Jansch L., Kruft V., Schmitz U.K., Braun H.P.;  
 RT "New insights into the composition, molecular mass and stoichiometry  
 RT of the protein complexes of plant mitochondria";  
 RL Plant J. 9:357-368(1996).  
 CC -!- FUNCTION: This protein seems to be part of the stalk that links  
 CC CF(0) to CF(1). It either transmits conformational changes from  
 CC CF(0) into CF(1) or is implicated in proton conduction.  
 CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +  
 CC H(+)(Out).  
 CC -!- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic  
 CC core - and CF(0) - the membrane proton channel. CF(1) has five  
 CC subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0)  
 CC has three main subunits: a, b and c.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial.  
 CC -!- SIMILARITY: Belongs to the ATPase delta chain family.  
 DR InterPro: IPR000711; APpynt\_OSCP.  
 DR PROSITE: PS00389; ATPASE\_DELTA; PARTIAL.  
 KW Hydrolyase; ATP synthesis; CF(1); Hydrogen ion transport;

KW Mitochondrion.  
 FT NON TER 37  
 SQ SEQUENCE 37 AA; 4003 MW; 9BFDAB14A298F4AF CRC64;  
 Query Match 100.0%; Score 21; DB 1; Length 37;  
 Best Local Similarity 100.0%; Pred. No. 32;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YVAD 4  
 Db 8 YVAD 11  
 RESULT 4  
 ID \_CUPI SARBU STANDARD; PRT; 43 AA.  
 AC P14485;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DE 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Larval cuticle protein SC1 (Fragment).  
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Sarcophagidae; Sarcophaga.  
 OX NCBI\_TaxID=7385;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=86037264; PubMed=3932663;  
 RA Henzel W.J., Mole J.E., Mullican K., Lipke H.;  
 RT "Sarcophagid larval proteins: partial sequence homologies among three  
 RT cuticle proteins and related structures of drosophilids";  
 RL J. Mol. Evol. 22:39-45(1985).  
 CC -!- FUNCTION: Component of the cuticle of the larva of flesh fly.  
 CC -!- SIMILARITY: Contains 1 cuticle consensus domain.  
 DR PIR: A24553; A24553.  
 DR InterPro: IPR000618; Insect cuticle.  
 DR Pfam: PFC0379; Chitin bind 4; 1.  
 DR PROSITE: PS00233; CUTICLE; PARTIAL.  
 KW Structural protein; Cuticle.  
 FT NON TER 43  
 SQ SEQUENCE 43 AA; 4556 MW; 6B3FD9A0B67E2210 CRC64;  
 Query Match 100.0%; Score 21; DB 1; Length 43;  
 Best Local Similarity 100.0%; Pred. No. 38;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YVAD 4  
 Db 39 YVAD 42  
 RESULT 5  
 ID RS18\_CHLTE STANDARD; PRT; 74 AA.  
 AC Q8KAM3;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DE 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE 30S ribosomal protein S18.  
 GN RPSR OR C72133.  
 OS Chlorobium tepidum.  
 OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;  
 OC Chlorobium.  
 OX NCBI\_TaxID=1097;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=TLS / ATCC 49652 / DSM 12025;  
 RX MEDLINE=22103685; PubMed=12093901;  
 RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,  
 RA Dodson R.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H.,  
 RA Hickey B.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,  
 RA Holt I., Unayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,

RA Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,  
RA Vamathavan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,  
RA Venter J.C., Tettelin H., Bryant D.A., Fraser C.M., Ketchum K.A.,  
RT "The complete genome sequence of *Chlorobium tepidum* TJS, a  
RT photosynthetic, anaerobic, green-sulfur bacterium";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514 (2002).  
CC -1- FUNCTION: Binds as a heterodimer with protein S6 to the central  
CC domain of the 16S rRNA, where it helps stabilize the platform of  
CC the 30S subunit (By similarity).  
CC -1- SUBUNIT: Part of the 30S ribosomal subunit. Forms a tight  
CC heterodimer with protein S6 (By similarity).  
CC -1- SIMILARITY: Belongs to the S18P family of ribosomal proteins.  
CC -----  
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CC -----  
CC EMBL; AE012962; AAM73349.1; --  
CC TIGR; CT2133; --  
CC HAMAP; MF 00270; --  
CC InterPro; IPR001648; Ribosomal\_S18.  
CC Pfam; PF01084; Ribosomal\_S18; 1.  
CC PRINTS; PR00974; RIBOSOMALS18.  
CC ProDom; PD002239; Ribosomal\_S18; 1.  
CC TIGRFAMs; TIGR00165; S18; 1.  
CC ProDom; PD002239; Ribosomal\_S18; 1.  
CC PROSITE; PS00057; RIBOSOMAL\_S18; FALSE NEG.  
CC Ribosomal protein; RNA-binding; rRNA-binding; Complete proteome.  
CC KW RIBOSOMAL PROTEIN; RNA-BINDING; RRNA-BINDING; Complete proteome.  
CC SEQUENCE 74 AA; 8671 MW; 71204A25284DE8B CRC64;

Query Match 100.0%; Score 21; DB 1; Length 74;  
Best Local Similarity 100.0%; Pred. No. 65;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
|||  
DB 68 YVAD 71

RESULT 6  
ID HPIS\_RHOPE STANDARD; PRT; 75 AA.  
AC P00882;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE High potential iron-sulfur protein (HiPIP).  
GN HIP.  
OS Rhodospirillum rubrum.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Comamonadaceae; Rhodospirillum.  
CC Comamonadaceae; Rhodospirillum.  
CC NCBI\_TaxID=28066;  
CC [1]  
CC SEQUENCE  
CC STRAIN=JMC 7819;  
CC MEDLINE=97234565; PubMed=9119002;  
CC van Briesche G., Chirli S., Hochkoeppler A., van Beeumen J.J.;  
RT "The primary structure of Rhodospirillum rubrum high-potential iron-  
RT sulfur protein, an electron donor to the photosynthetic reaction  
RT center";  
RT Eur. J. Biochem. 244:371-377 (1997).  
CC -1- FUNCTION: Specific class of high-redox-potential 4Fe-4S  
CC ferredoxins. Functions in anaerobic electron transport in most  
CC purple and in some other photosynthetic bacteria and in at least  
CC one genus (Paracoccus) of halophilic, denitrifying bacteria.  
CC -1- SUBUNIT: Homodimer (By similarity).  
CC -1- MASS SPECTROMETRY: MW=7849.64; METHOD=Electrospray.  
CC -1- SIMILARITY: Belongs to the high potential iron-sulfur protein  
CC (HiPIP) family.  
CC HSP; P00260; 1CKU.

DR InterPro; IPR000170; Hipot\_iron\_sulf.  
DR Pfam; PF01355; HiPIP; 1.  
DR PROSITE; PS00596; HiPIP; 1.  
KW Electron transport; Iron-sulfur; 4Fe-4S.  
FT METAL 38 38 IRON-SULFUR (4FE-4S) (BY SIMILARITY).  
FT METAL 41 41 IRON-SULFUR (4FE-4S) (BY SIMILARITY).  
FT METAL 54 54 IRON-SULFUR (4FE-4S) (BY SIMILARITY).  
FT METAL 68 68 IRON-SULFUR (4FE-4S) (BY SIMILARITY).  
FT METAL 75 75 IRON-SULFUR (4FE-4S) (BY SIMILARITY).  
SQ SEQUENCE 75 AA; 7849 MW; 9F8C8662A72D3 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 75;  
Best Local Similarity 100.0%; Pred. No. 66;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
|||  
DB 17 YVAD 20

RESULT 7  
ID RS18\_BACST STANDARD; PRT; 77 AA.  
AC P10806;  
DT 01-JUL-1989 (Rel. 11, Created)  
DT 01-JUL-1989 (Rel. 11, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE 30S ribosomal protein S18 (BS21) (BS19).  
GN RPSR.  
OS Bacillus stearothermophilus.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.  
CC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.  
CC NCBI\_TaxID=1422;  
CC [1]  
CC SEQUENCE.  
CC STRAIN=799;  
CC MEDLINE=89171319; PubMed=2647521;  
CC McDougall J., Choli T., Kruff V., Kapp U., Wittmann-Liebold B.;  
RT "The complete amino acid sequence of ribosomal protein S18 from the  
RT moderate thermophile *Bacillus stearothermophilus*.";  
RL FEBS Lett. 245:253-260 (1989).  
CC [2]  
CC SEQUENCE OF 1-15.  
CC STRAIN=10;  
CC MEDLINE=75019590; PubMed=4607606;  
CC Yaguchi M., Matheson A.T., Visentin L.P.;  
RT "Prokaryotic ribosomal proteins: N-terminal sequence homologies and  
RT structural correspondence of 30 S ribosomal proteins from *Escherichia*  
RT coli and *Bacillus stearothermophilus*.";  
RL FEBS Lett. 46:296-300 (1974).  
CC -1- FUNCTION: Binds as a heterodimer with protein S6 to the central  
CC domain of the 16S rRNA, where it helps stabilize the platform of  
CC the 30S subunit (By similarity).  
CC -1- SUBUNIT: Part of the 30S ribosomal subunit. Forms a tight  
CC heterodimer with protein S6 (By similarity).  
CC -1- SIMILARITY: Belongs to the S18P family of ribosomal proteins.  
CC PIR; S03556; R3BS18.  
CC HAMAP; MF 00270; --  
CC InterPro; IPR001648; Ribosomal\_S18.  
CC Pfam; PF01084; Ribosomal\_S18; 1.  
CC PRINTS; PR00974; RIBOSOMALS18.  
CC ProDom; PD002239; Ribosomal\_S18; 1.  
CC TIGRFAMs; TIGR00165; S18; 1.  
CC PROSITE; PS00057; RIBOSOMAL\_S18; 1.  
CC Ribosomal protein; RNA-binding; rRNA-binding.  
CC INIT MET 0  
CC SEQUENCE 77 AA; 8837 MW; A3F635FC64210E42 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 77;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
|||  
DB 73 YVAD 76

RESULT 8  
Y467\_TREPA STANDARD; PRT; 82 AA.  
AC O83480;  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein TP0467.  
GN TP0467.  
OS Treponema pallidum.  
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.  
OX NCBI\_TaxID=160;  
[1]  
SEQUENCE FROM N.A.  
RC STRAIN=Nichols;  
RX MEDLINE=98332770; PubMed=9665876;  
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,  
RA Dodson R., Gwin M., Hickey E.K., Clayton R., Ketchum K.A.,  
RA Sodergren B., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,  
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,  
RA McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,  
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,  
RA Venter J.C.;  
RT "Complete genome sequence of Treponema pallidum, the syphilis  
RT spirochete.";  
RL Science 281:375-388(1998).  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; AB001223; AAC65458.1; -  
DR PIR; E71321; E71321.  
DR TIGR; TP0467; -  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 82 AA; 9614 MW; FDA6ACAE370890C CRC64;  
  
Query Match 100.0%; Score 21; DB 1; Length 82;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 YVAD 4  
DB 31 YVAD 34  
  
RESULT 9  
YQGV\_BACSU STANDARD; PRT; 94 AA.  
AC P54459;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Hypothetical protein YQGV.  
GN YQGV OR BSU24810.  
OS Bacillus subtilis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1423;  
[1]  
SEQUENCE FROM N.A.  
RC STRAIN=168 / JH642;  
RX MEDLINE=97124195; PubMed=6969508;  
RA Mizuno M., Mauda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,  
RA Kobayashi Y.;  
RT "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of  
RT the Bacillus subtilis genome containing the skin element and many  
RT sporulation genes.";  
  
Microbiology 142:3103-3111(1996).  
[2]  
SEQUENCE FROM N.A.  
RX STRAIN=168;  
RX MEDLINE=98044033; PubMed=9384377;  
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., S.,  
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,  
RA Boriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,  
RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,  
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,  
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,  
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,  
RA Friz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,  
RA Chim S.Y., Glaser P., Goffeau A., Gligitsky E.J., Grandi G.,  
RA Guiseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,  
RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,  
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,  
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,  
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,  
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,  
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,  
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudga B., Park S.H.,  
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,  
RA Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,  
RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadale Y.,  
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,  
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,  
RA Srokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,  
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,  
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,  
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,  
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,  
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;  
RT "The complete genome sequence of the Gram-positive bacterium Bacillus  
RT subtilis.";  
RL Nature 390:249-256(1997).  
CC -----  
CC -!- SIMILARITY: BELONGS TO THE UPF0045 FAMILY.  
CC -----  
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CC -----  
CC EMBL; D84432; BAA12525.1; -  
DR PIR; G69957; G69957.  
DR Subtilist; BG11689; YQGV.  
DR InterPro; IPR002787; DUF77.  
DR Pfam; PF01910; DUF77; 1.  
DR TIGRFAMS; TIGR00106; TIGR00106; 1.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 94 AA; 10453 MW; 4A576F2338B80999 CRC64;  
  
Query Match 100.0%; Score 21; DB 1; Length 94;  
Best Local Similarity 100.0%; Pred. No. 83;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 YVAD 4  
DB 21 YVAD 24  
  
RESULT 10  
CPAL\_CANFG STANDARD; PRT; 102 AA.  
ID CPAL\_CANFG  
AC P81575;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cuticle protein AM/CP114 (CPAM/CPAM114).

OS Cancer pagurus (Rock crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubranchyura; Cancroidea; Cancridae; Cancer.  
OX NCBI\_TaxID=6755;  
RN [1]  
RN SEQUENCE.  
RP TISSUE=Carapace cuticle;  
RX MEDLINE=99354472; PubMed=10425740;  
RA Andersen S.O.;  
RL "Exoskeletal proteins from the crab, Cancer pagurus";  
RT Comp. Biochem. Physiol. 123A:203-211(1999).  
CC -!- TISSUE SPECIFICITY: Arthroclial membrane and calcified shell.  
CC -!- MASS SPECTROMETRY: MW=11139.8; METHOD=WALDI.  
CC -!- SIMILARITY: Contains 1 cuticle consensus domain.  
DR InterPro; IPR000618; Insect cuticle.  
DR Pfam; PF00379; Chitin\_bind\_4; 1.  
DR PRINTS; PR00947; CUTICLE.  
DR PROSITE; PS00233; CUTICLE; FALSE\_NEG.  
KW Structural protein; Cuticle.  
SQ SEQUENCE 102 AA; 11142 MW; 17101253BF109533 CRC64;  
  
Query Match 100.0%; Score 21; DB 1; Length 102;  
Best Local Similarity 100.0%; Pred. No. 90;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 YVAD 4  
DB 63 YVAD 66  
|||||  
  
RESULT 11  
LCPS\_DROME STANDARD; PRT; 104 AA.  
ID LCPS\_DROME  
AC P92192; O96905;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Larval cuticle protein V precursor.  
GN (LCP65A1 OR LCP5 OR DCP3-ALPHA OR CG18776) AND  
GN (LCP65A2 OR LCP5 OR DCP3-BETA OR CG18773).  
OS Drosophila melanogaster (fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=Oregon-R;  
RC Mandalaparth P., Jiang S., Schneider G., Chihara C.;  
RT "The cuticle proteins of Drosophila melanogaster: sequence of Lcp5 in  
RT the third chromosome cluster."  
RL Dros. Info. Service 77:49-51(1996).  
RN [2]  
RN SEQUENCE FROM N.A.  
RP STRAIN=Iso-1;  
RX MEDLINE=98043412; PubMed=9383064;  
RA Charles J.-P., Chihara C., Nejad S., Riddiford L.M.;  
RT "A cluster of cuticle genes of Drosophila at 65A: sequence, structure  
RT and evolution."  
RL Genetics 147:1213-1224(1997).  
RN [3]  
RN SEQUENCE FROM N.A.  
RP STRAIN=Berkley;  
RC Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RX Ananides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,  
RA George R.A., Lewis S.E., Wendell M.D., Zhang Q., Chen L.X.,  
PA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Agbayani A., An H.-U., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
Fowler C., Gabrielian A.E., Garg N.S., Gebart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Laslo P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J.J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster."  
RL Science 287:2185-2195(2000).  
RN [4]  
RN SEQUENCE FROM N.A.  
RP STRAIN=Berkley;  
RX MEDLINE=22426066; PubMed=12537569;  
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M., Wan K.H.,  
RA George R.A., Guarini H., Kronmiller B., Pacleb J.M., Park S.,  
RA Rubin G.M., Celniker S.E.;  
RT "A Drosophila full-length cDNA resource."  
RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).  
RN [5]  
RN SEQUENCE OF 19-32.  
RP STRAIN=Oregon-R; TISSUE=Larva;  
RX MEDLINE=98318806; PubMed=9654737;  
RA Charles J.-P., Chihara C., Nejad S., Riddiford L.M.;  
RT "Identification of proteins and developmental expression of RNAs  
RT encoded by the 65A cuticle protein gene cluster in Drosophila  
RT melanogaster."  
RL Insect Biochem. Mol. Biol. 28:131-138(1998).  
CC -!- FUNCTION: Component of the cuticle of the larva.  
CC -!- SIMILARITY: Contains 1 cuticle consensus domain.  
CC -----  
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CC -----  
DR EMBL; U81550; AAB00301.1; -;  
DR EMBL; U84746; AAB88065.1; -;  
DR EMBL; U84747; AAB88066.1; -;  
DR EMBL; A5003563; AAG22328.1; -;  
DR EMBL; A5003563; AAG22331.1; -;  
DR EMBL; AY071366; AAL48988.1; -;  
DR FlyBase; FBgn020644; Lcp65Ab1.  
DR FlyBase; FBgn020643; Lcp65Ab2.  
DR InterPro; IPR000618; Insect cuticle.  
DR Pfam; PF00379; Chitin\_bind\_4; 1  
DR PROSITE; PS00233; CUTICLE; FALSE\_NEG.  
KW Structural protein; Cuticle; Signal.  
FT SIGNAL 1 18  
FT CHAIN 19 104 LARVAL CUTICLE PROTEIN V.

FT	CONFLICT	52	72	AAVHGSFTWV -> CRCPRILHLG (IN REF. 1).
SEQ	SEQUENCE	104 AA;	11267 MW;	BA60DD9483DD6992 CRC64;
Query Match	100.0%;	Score 21;	DB 1;	Length 104;
Best Local Similarity	100.0%;	Pred. NO. 92;		
Matches	4;	Conservative	0;	Mismatches 0; Indels 0; Gaps
QY	1 YVAD 4			
DB	84 YVAD 87			
RESULT 12				
CPA2_CANPG				
ID	_CPA2_CANPG	STANDARD;	PRT;	105 AA.
AD	P81576;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Cuticle protein AML159 (CPAM1159).			
DE	Cancer pagurus (Rock crab).			
OC	Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;			
OC	Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;			
OC	Eubrachyura; Cancroidea; Cancridae; Cancer.			
OX	NCBI_TaxID=6755;			
RN	[1]			
SEQ	SEQUENCE.			
RC	TISSUE=Carapace cuticle;			
RC	MEDLINE=99354472; PubMed=10425740;			
RA	Andersen S.O.;			
RA	"Exoskeletal proteins from the crab, Cancer pagurus.";			
RL	Comp. Biochem. Physiol. 123A:203-211(1999).			
CC	-!- TISSUE SPECIFICITY: Arthropodial membrane.			
CC	-!- MASS SPECTROMETRY: MW=11582.8; METHOD=MALDI.			
CC	-!- SIMILARITY: Contains 1 cuticle consensus domain.			
CC	InterPro; IPR000618; Insect cuticle.			
DR	Ficaf; PF00379; Chitin bind_4; 1.			
DR	PRINTS; PRO0947; CUTICLE.			
DR	PROSITE; PS00233; CUTICLE; 1.			
KW	Structural protein; Cuticle.			
SEQ	SEQUENCE 105 AA; 11586 MW; 6C8827FA4E149729 CRC64;			
Query Match	100.08;	Score 21;	DB 1;	Length 105;
Best Local Similarity	100.08;	Pred. NO. 93;		
Matches	4;	Conservative	0;	Mismatches 0; Indels 0; Gaps
QY	1 YVAD 4			
DB	63 YVAD 66			
RESULT 13				
YU90_MYCTU				
ID	_YU90_MYCTU	STANDARD;	PRT;	113 AA.
AD	Q10868;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Hypothetical protein Rv1990c/MT2044/Mb2012c precursor.			
GN	Rv1990C OR MT2044 OR MTCY39.29 OR MB2012C.			
OS	Mycobacterium tuberculosis, and			
OS	Mycobacterium bovis.			
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;			
OC	Corynebacterineae; Mycobacteriaceae; Mycobacterium.			
OX	NCBI_TaxID=1773; 1765;			
RN	[1]			
SEQ	SEQUENCE FROM N.A.			
RC	SPECIES=M.tuberculosis; STRAIN=H37Rv;			
RC	MEDLINE=98295987; PubMed=9634230;			
RA	Cole S.T.; Broesch R.; Parkhill J.; Garnier T.; Churcher C.; Harris D.			
RA	Gordon S.V.; Eiglmeier K.; Gas S.; Barry C.E. III; Tekala F.;			
RA	Badcock K.; Basham D.; Brown D.; Chillingworth T.; Connor R.;			
RA	Davies R.; Devlin K.; Feltwell T.; Gentles S.; Hamlin N.; Holroyd S.			

Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrett B.G.; Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence." ; Nature 393:537-544(1998).

[2]

SEQUENCE FROM N.A.

RK SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oehkosh;

RC MEDLINE=22026494; PubMed=12218036;

RX Fleischmann R.D., Allard D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; Whole-genome comparison of Mycobacterium tuberculosis clinical and laboratory strains."; RT J. Bacteriol. 184:5479-5490(2002).

[3]

SEQUENCE FROM N.A.

RN SPECIES=M.bovis; STRAIN=AF2122/97;

RP MEDLINE=22709107; PubMed=12788972;

RC Garnier T., Biglmeier K., Camus J.-C., Medina N., Mansour H., Pivrot M., Duchoy S., Grondin S., Lacroix C., Monsemp C., Simon S., Harris B., Atkin R., Doggett J., Hayes R., Keating L., Wheeler P.R., Parkhill J., Barrall B.G., Cole S.T., Gordon S.V., Hewinson R.G.; The complete genome sequence of Mycobacterium bovis."; RT Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).

CC

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CC

EMBL: Z74025; CAA98394.1; --

DR EMBL: AE007056; AAK46320.1; --

DR EMBL: BX248341; CAD9685.1; --

DR PIR: D70757; D70757.

DR TIGR: MT2044; --

DR Tuberculinist; Rv1990c; --

DR Hypothetical protein; Signal; Complete proteome.

KW Hypothetical protein; 13 POTENTIAL.

FT SIGNAL 1 13

FT CHAIN 14 113

FT HYPOTHEITICAL PROTEIN RVI990C/MT2044/NB2012C.

FT FT

SEQ SEQUENCE 113 AA; 12488 MW; 41978D1BE45E74C9 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 113;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVAD 4

Db 58 YVAD 61

|||||

RESULT 14

GLHA\_ACALA ID GLHA\_ACALA STANDARD; PRT; 117 AA.

AC F30970;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE Glycoprotein hormones alpha chain precursor (Gonadotropin alpha chain) (GTH-alpha).

DE Os Acanthopagrus latus (Yellowfin porry).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Percoidae; Sparidae; Acanthopagrus.

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OX NCBI_TaxID=8177;
RN [1]
RP SEQUENCE FROM N.A.
RA Tsai H.J., Chen Y.L.;
RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in gametogenesis and steroidogenesis.
CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the glycoprotein hormones alpha chain
CC family.
CC
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CC
CC -----
CC EMBL; M94038; AAA48513.1; -.
CC HSP; P01215; 1XUL.
CC InterPro: IPR002400; GF_CysKnot.
CC InterPro: IPR000476; Glyco_hormone.
CC Pfam; PF00236; hormone6; 1.
CC PRINTS; PRO0438; GFCYSKNOT.
CC PRINTS; PRO0274; GLYCOHORMONE.
CC ProDom; PD002047; Glyco_hormone; 1.
CC SMART; SM00067; GHA; 1.
CC PROSITE; PS00779; GLYCO_HORMONE_ALPHA_1; 1.
CC PROSITE; PS00780; GLYCO_HORMONE_ALPHA_2; 1.
CC PROSITE; PS50277; GLYCO_HORMONE_ALPHA_3; 1.
KW Hormone; Glycoprotein; Signal.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 117 GLYCOPROTEIN HORMONES ALPHA CHAIN.
FT DISULFID 34 57 BY SIMILARITY.
FT DISULFID 37 86 BY SIMILARITY.
FT DISULFID 54 107 BY SIMILARITY.
FT DISULFID 58 109 BY SIMILARITY.
FT DISULFID 55 112 BY SIMILARITY.
FT CARBOHYD 78 78 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 103 103 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 117 AA; 13061 MW; F9ACE213DB67AF14 CRC64;
Query Match 100.0%; Score 21; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
Db 19 YVAD 22

RESULT 15
TVB5_MOUSE
ID TVB5_MOUSE STANDARD; PRT; 122 AA.
AC P04213;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE T-cell receptor beta chain V region C5 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85036636; PubMed=6092964;
RA Fatten P., Yokota T., Rothbard J., Chien Y., Arai K., Davis M.M.;
RT "Structure, expression and divergence of T-cell receptor beta-chain
RT variable regions."
RL Nature 312:40-46(1984).
CC -!- MISCELLANEOUS: This sequence was derived from a T-helper clone.
CC PIR; A02008; RMSCS.
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DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW T-cell; Receptor; Immunoglobulin domain; Signal.
FT NON_TER 1 1
FT SIGNAL <1 7
FT CHAIN 8 122 T-CELL RECEPTOR BETA CHAIN V REGION C5.
FT DOMAIN 8 103 V SEGMENT.
FT DOMAIN 104 108 D SEGMENT.
FT DOMAIN 109 122 J SEGMENT.
FT DISULFID 31 99 BY SIMILARITY.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13349 MW; D657DCC9B261C64C CRC64;
Query Match 100.0%; Score 21; DB 1; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
Db 58 YVAD 61

Search completed: May 24, 2004, 14:39:33
Job time : 11.5 secs
```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 24, 2004, 14:36:17 ; Search time 36.5 Seconds  
(without alignments)  
34.577 Million cell updates/sec

Title: US-09-765-105A-1  
Perfect score: 21  
Sequence: 1 YVAD 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL.25.\*

- 1: sp\_arChaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	21	100.0	32	Q868A6	Q868A6 drosophila
2	21	100.0	44	11 Q8BJM4	Q8bjm4 mus musculu
3	21	100.0	45	9 Q858A7	Q858a7 mycobacteri
4	21	100.0	51	7 Q7VP64	Q7vp64 aethia cris
5	21	100.0	52	7 Q31335	Q31335 alligator m
6	21	100.0	52	7 Q31337	Q31337 alligator m
7	21	100.0	53	7 Q8SNE1	Q8snel gallinago m
8	21	100.0	54	16 Q9PE99	Q9pe99 xylella fas
9	21	100.0	62	16 Q8Y145	Q8y145 ralstonia s
10	21	100.0	62	16 Q8XSA4	Q8ksa4 ralstonia s
11	21	100.0	65	16 Q89DP2	Q89dp2 bradyrhizob
12	21	100.0	66	2 Q85X3	Q85x3 streptococ
13	21	100.0	66	6 P73275	P73275 sus scrofa
14	21	100.0	66	7 Q8SP36	Q8sp36 pygoscelis
15	21	100.0	66	7 Q8SP52	Q8sp52 pygoscelis
16	21	100.0	66	7 Q8SP50	Q8sp50 pygoscelis

ALIGNMENTS

RESULT 1

Q868A6 PRELIMINARY; PRT; 32 AA.

ID Q868A6  
AC Q868A6;  
DT 01-JUN-2003 (TREMBlrel. 24, Created)  
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Alcohol dehydrogenase related protein (Fragment).  
GN ADHR.

OS Drosophila miranda (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7229;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=0101.3, 0101.4, 0101.5, 0101.7, 0101.9, MA32, MA28, SPI38,  
RC SP235, SP295, MSH22, and MSH38;  
RA Yi S., Bachtrog D., Charlesworth B.;  
RT "A survey of chromosomal and nucleotide sequence variation in  
RT Drosophila miranda";  
RL Genetics 0.0-0(2003);  
DR EMBL; AY238770; AAC84926.1; -  
DR EMBL; AY238771; AAC84928.1; -  
DR EMBL; AY238772; AAC84930.1; -  
DR EMBL; AY238773; AAC84932.1; -  
DR EMBL; AY238774; AAC84934.1; -  
DR EMBL; AY238775; AAC84936.1; -  
DR EMBL; AY238776; AAC84938.1; -  
DR EMBL; AY238777; AAC84940.1; -  
DR EMBL; AY238778; AAC84942.1; -  
DR EMBL; AY238779; AAC84944.1; -  
DR EMBL; AY238780; AAC84946.1; -  
DR EMBL; AY238781; AAC84948.1; -  
FT NON TER 32  
SQ SEQUENCE 32 AA; 3446 MW; 0F0D949AFCBE63BE CRC64;

Query Match 100.0%; Score 21; DB 5; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;



Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
11 YVAD 14

Db

RESULT 2

Q8BJM4 PRELIMINARY; PRT; 44 AA.

ID Q8BJM4  
AC Q8BJM4  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Protein kinase C-like 2 (Fragment).  
GN 6030436C20RIK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Body;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs";  
RL Nature 420:563-573 (2002).  
DR EMBL; AK082921; BAC38889.1; -  
DR MGD; MGI:1925929; 6030436C20RIK.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000961; Pkinase\_C.  
DR Pfam; PF00433; Pkinase\_C; 1.  
FT NON\_TER 1  
SQ SEQUENCE 44 AA; 5277 MW; FF86B72F23FF8AB2 CRC64;

Query Match 100.0%; Score 21; DB 11; Length 44;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
39 YVAD 42

Db

RESULT 3

Q858A7 PRELIMINARY; PRT; 45 AA.

ID Q858A7  
AC Q858A7  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Gp4.  
OS Mycobacteriophage Cjw1.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.  
OX NCBI\_TaxID=205869;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22592660; PubMed=12705866;  
RA Pedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C.,  
RA Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pannunzio N.R.,  
RA Brucker W., Kumar V., Kandasamy J., Xenan L., Bardarov S.,  
RA Krizakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,  
RA Hatfull G.F.;  
RT "Origins of highly mosaic mycobacteriophage genomes.";  
RL Cell 113:171-182 (2003).  
DR EMBL; AY129331; AAN01619.1; -  
SQ SEQUENCE 45 AA; 5310 MW; DDE073829E591F73 CRC64;

Query Match 100.0%; Score 21; DB 9; Length 45;

Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
6 YVAD 9

Db

RESULT 4

Q7YF64 PRELIMINARY; PRT; 51 AA.

ID Q7YF64  
AC Q7YF64  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE MHC class II antigen B (Fragment).  
GN Aethia cristatella (Crested auklet).  
OS Aethia cristatella (Crested auklet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Charadriiformes; Alcidae; Aethia.  
OX NCBI\_TaxID=28685;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC Walsh H.E., Friesen V.L.;  
RT "A comparison of intra-specific patterns of DNA sequence variation in  
RT Mitochondrial DNA, a-Enolase, and MHC Class II B loci in Auklets  
(Charadriiformes: Alcidae).";  
RT Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
RL EMBL; AY327429; AAP93579.1; -  
FT NON\_TER 1  
FT NON\_TER 51  
SQ SEQUENCE 51 AA; 5834 MW; 51AD1C39EF56C3EC CRC64;

Query Match 100.0%; Score 21; DB 7; Length 51;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4  
4 YVAD 7

Db

RESULT 5

Q31335 PRELIMINARY; PRT; 52 AA.

ID Q31335  
AC Q31335  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE MHC class II B protein (Fragment).  
GN MHC CLASS II B.  
OS Alligator mississippiensis (American alligator).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.  
OX NCBI\_TaxID=8496;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=American alligator; TISSUE=Blood;  
RX MEDLINE=96137171; PubMed=8564010;  
RA Edwards S.V., Grann M., Potts W.K.;  
RT "Dynamics of Mhc evolution in birds and crocodilians: amplification of  
class II genes with degenerate primers";  
RL MGI. Scol. 4:719-729 (1995).  
DR EMBL; U24402; AAA99113.1; -  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0045012; F:MHC class II receptor activity; IEA.  
DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.  
DR GO; GO:0019886; P:antigen processing, exogenous antigen via M. . .; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR000353; MHC\_II\_beta.  
DR Pfam; PF00969; MHC\_II\_beta; 1.  
DR ProDom; PD000328; MHC\_II\_beta; 1.  
DR Glycoprotein; MHC II; Transmembrane.  
FT NON\_TER 1

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FT NON_TER 52 52
SQ SEQUENCE 52 AA; 6198 MW; D5405DA025C11698 CRC64;

Query Match 100.0%; Score 21; DB 7; Length 52;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
Db 24 YVAD 27

RESULT 6
Q31337 PRELIMINARY; PRT; 52 AA.
AC Q31337;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC class II B protein (Fragment).
GN MHC CLASS II B.
OS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX NCBI_TaxID=8496;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=American alligator; TISSUE=Blood;
RX MEDLINE=9613771; PubMed=8564010;
RA Edwards S.V., Gram M., Potts W.K.;
RT "Dynamics of Mhc evolution in birds and crocodilians: amplification of
class II genes with degenerate primers.";
RL Mol. Ecol. 4:719-729(1995).
DR EMBL; U24404; AAA9115.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0045012; F: MHC class II receptor activity; IEA.
DR GO; GO:0019884; P: antigen presentation, exogenous antigen; IEA.
DR GO; GO:0019886; P: antigen processing, exogenous antigen via M. . .; IEA.
DR GO; GO:0006955; P: immune response; IEA.
DR InterPro; IPR000353; MHC II beta.
DR Pfam; PF00969; MHC II beta; 1.
DR ProDom; PD000328; MHC II beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1 1
FT NON_TER 52 52
SQ SEQUENCE 52 AA; 6199 MW; D84EBDA025C11698 CRC64;

Query Match 100.0%; Score 21; DB 7; Length 52;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
Db 24 YVAD 27

RESULT 7
Q8SNE1 PRELIMINARY; PRT; 53 AA.
AC Q8SNE1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC class II antigen B (Fragment).
OS Gallinago media (great snipe).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Charadriiformes; Scolopacidae;
OC Gallinago.
OX NCBI_TaxID=114734;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=gall 6;
RA Ekblom R., Grahn M., Hoglund J.;

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RT "Patterns of polymorphism in the MHC class II of a non-passerine bird,
the great snipe (Gallinago media).";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF485412; AAL93175.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0045012; F: MHC class II receptor activity; IEA.
DR GO; GO:0019884; P: antigen presentation, exogenous antigen; IEA.
DR GO; GO:0019886; P: antigen processing, exogenous antigen via M. . .; IEA.
DR GO; GO:0006955; P: immune response; IEA.
DR InterPro; IPR000353; MHC II beta.
DR Pfam; PF00969; MHC II beta; 1.
DR ProDom; PD000328; MHC II beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1 1
FT NON_TER 53 53
SQ SEQUENCE 53 AA; 6235 MW; F8A0B0E3C316727 CRC64;

Query Match 100.0%; Score 21; DB 7; Length 53;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVAD 4
Db 26 YVAD 29

RESULT 8
Q9PE99 PRELIMINARY; PRT; 54 AA.
AC Q9PE99;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein Xf1129.
GN Xf1129.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9a5c;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferzo J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.P.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.B.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuchiko M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL; AF003949; AAF83939.1; -.
DR FIR; H82718; H82718.

```

KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 54 AA; 5864 MW; F1B7B7C4B250C4B7 CRC64;  
Query Match 100.0%; Score 21; DB 16; Length 54;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YVAD 4  
DB 50 YVAD 53  
RESULT 9  
Q8Y145 ID Q8Y145 PRELIMINARY; PRT; 62 AA.  
AC Q8Y145;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Hypothetical protein RSC0848.  
GN RSC0848 OR RS06110.  
OS Ralstonia solanacearum (Pseudomonas solanacearum).  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Burkholderiaceae; Ralstonia.  
OX NCBI\_TaxID=305;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GM11000;  
RX MEDLINE=21681879; PubMed=11823852;  
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,  
RA Ariat M., Billault A., Brottier P., Camus J.C., Catolico L.,  
RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Denange N.,  
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,  
RA Sigulier P., Thebaud P., Whalen M., Wincker P., Levy M.,  
RA Weissbach J., Boucher C.A.;  
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";  
KL Nature 415:497-502(2002).  
DR EMBL: AL646061; CAD14550.1; -;  
SQ SEQUENCE 62 AA; 6788 MW; 3AAC89CAC50B44F3 CRC64;  
Query Match 100.0%; Score 21; DB 16; Length 62;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YVAD 4  
DB 46 YVAD 49  
RESULT 10  
Q8XSA4 ID Q8XSA4 PRELIMINARY; PRT; 62 AA.  
AC Q8XSA4;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein RSP0574.  
GN RSP0574 OR RS06111.  
OS Ralstonia solanacearum (Pseudomonas solanacearum).  
OC Plasmid megaplasmid.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Burkholderiaceae; Ralstonia.  
OX NCBI\_TaxID=305;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GM11000;  
RX MEDLINE=21681879; PubMed=11823852;  
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,  
RA Ariat M., Billault A., Brottier P., Camus J.C., Catolico L.,  
RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Denange N.,  
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,  
RA Sigulier P., Thebaud P., Whalen M., Wincker P., Levy M.,  
RA Weissbach J., Boucher C.A.;  
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";  
KL Nature 415:497-502(2002).  
DR EMBL: AL646061; CAD14550.1; -;  
SQ SEQUENCE 62 AA; 6788 MW; 3AAC89CAC50B44F3 CRC64;  
Query Match 100.0%; Score 21; DB 16; Length 62;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YVAD 4  
DB 46 YVAD 49

RA Weissbach J., Boucher C.A.;  
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";  
KL Nature 415:497-502(2002).  
DR EMBL: AL646079; CAD17725.1; -;  
DR GO: GO:0046821; C:extrachromosomal DNA; IEA.  
KW Plasmid; Hypothetical protein; Complete proteome.  
SQ SEQUENCE 62 AA; 6474 MW; DA5BA57B43B87664 CRC64;  
Query Match 100.0%; Score 21; DB 16; Length 62;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YVAD 4  
DB 46 YVAD 49  
RESULT 11  
Q89DP2 ID Q89DP2 PRELIMINARY; PRT; 65 AA.  
AC Q89DP2;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Bsl7397 protein.  
GN Bsl7397.  
OS Bradyrhizobium japonicum.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Bradyrhizobiaceae; Bradyrhizobium.  
OX NCBI\_TaxID=375;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=USDA 110.  
RX MEDLINE=22484998; PubMed=12597275;  
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,  
RA Kawanoto S., Watarabe A., Ideawa K., Iiguchi M., Kawashima K.,  
RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,  
RA Tabata S.;  
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium  
Bradyrhizobium japonicum USDA110.";  
KL DNA Res. 9:189-197(2002).  
DR EMBL: AF005962; BAC52662.1; -;  
KW Complete proteome.  
SQ SEQUENCE 65 AA; 7091 MW; 4D8D7C3F9145F7B9 CRC64;  
Query Match 100.0%; Score 21; DB 16; Length 65;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YVAD 4  
DB 12 YVAD 15  
RESULT 12  
Q9RSX3 ID Q9RSX3 PRELIMINARY; PRT; 66 AA.  
AC Q9RSX3;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Penicillin-binding protein 2B, PBP 2B (Fragment).  
OS Streptococcus pneumoniae.  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
OC Streptococcus.  
OX NCBI\_TaxID=1313;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=94350848; PubMed=8071243;  
RA Hakenbeck R., Martin C., Dowson C., Grebe T.;  
RT "Penicillin-binding protein 2B of Streptococcus pneumoniae in  
piperacillin-resistant laboratory mutants.";  
KL J. Bacteriol. 176:5574-5577(1994).

DR GO; GO:0008658; F:penicillin binding; IEA.  
 DR GO; GO:0009273; P:cell wall biosynthesis (sensu Bacteria); IEA.  
 DR InterPro; IPR001460; Transpeptidase.  
 DR Pfam; PF00905; Transpeptidase; 1.  
 FT NON\_TER 1 66  
 FT NON\_TER 66  
 SQ SEQUENCE 66 AA; 7089 MW; 673DA1BCEC74B980 CRC64;  
 Query Match 100.0%; Score 21; DB 2; Length 66;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YVAD 4  
 DB 8 YVAD 11  
 RESULT 13  
 P79275 PRELIMINARY; PRT; 66 AA.  
 AC P79275;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Rho A (Fragment).  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=domestic; TISSUE=Pulmonary vein;  
 RX MEDLINE=97040892; PubMed=8986005;  
 RA Nishimura J., Sakihara C., Zhou Y., Kanaide H.;  
 RT "Expression of Rho A and Rho-kinase mRNAs in Porcine Vascular Smooth  
 Muscle.";  
 RL Biochem. Biophys. Res. Commun. 227:750-754 (1996).  
 DR ENBL; D89492; BAA13966.1; -.  
 DR PIR; PC4222; PC4222.  
 DR HSSP; P06749; 1FTN.  
 DR GO; GO:0008525; F:GTP binding; IEA.  
 DR GO; GO:000925; F:small monomeric GTPase activity; IEA.  
 DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.  
 DR InterPro; IPR001806; Ras\_transfrmg.  
 DR Pfam; PF00071; ras; 1.  
 KW GTP-binding.  
 FT NON\_TER 1 66  
 FT NON\_TER 66  
 SQ SEQUENCE 66 AA; 7562 MW; 38C71B220AD67C30 CRC64;  
 Query Match 100.0%; Score 21; DB 6; Length 66;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YVAD 4  
 DB 7 YVAD 10  
 RESULT 14  
 Q8SP36 PRELIMINARY; PRT; 66 AA.  
 AC Q8SP36;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE MHC class II antigen (Fragment).  
 GN PYR1.10.  
 OS Pygoscelis papua (Gentoo penguin).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Sphenisciformes; Spheniscidae;  
 OC Pygoscelis.  
 OX NCBI\_TaxID=30457;

RN SEQUENCE FROM N.A.  
 RX MEDLINE=21655119; PubMed=11797106;  
 RA Tsuda T.T., Tsuda M., Naruse T., Kawata H., Ando A., Shiina T.,  
 RA Fukuda M., Kurita M., Lemaho I., Kulski J.K., Inoko H.;  
 RT "Phylogenetic analysis of penguin(Spheniscidae) species based on  
 sequence variation in MHC class II genes.";  
 RL Immunogenetics 53:712-716(2001).  
 DR ENBL; AB043599; BAB86830.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0045012; F:MHC class II receptor activity; IEA.  
 DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.  
 DR GO; GO:0019886; P:antigen processing, exogenous antigen; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR000353; MHC\_II\_beta.  
 DR Pfam; PF00969; MHC\_II\_beta; 1.  
 DR ProDom; PD000328; MHC\_II\_beta; 1.  
 KW Glycoprotein; MHC II; Transmembrane.  
 FT NON\_TER 1 66  
 FT NON\_TER 66  
 SQ SEQUENCE 66 AA; 7774 MW; A955F9736710EADF CRC64;  
 Query Match 100.0%; Score 21; DB 7; Length 66;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YVAD 4  
 DB 29 YVAD 32  
 RESULT 15  
 Q8SP52 PRELIMINARY; PRT; 66 AA.  
 ID Q8SP52;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Major histocompatibility complex (Fragment).  
 GN PYAN1.01.  
 OS Pygoscelis antarctica (Chinstrap penguin).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Sphenisciformes; Spheniscidae;  
 OC Pygoscelis.  
 OX NCBI\_TaxID=79643;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21655119; PubMed=11797106;  
 RA Tsuda T.T., Tsuda M., Naruse T., Kawata H., Ando A., Shiina T.,  
 RA Fukuda M., Kurita M., Lemaho I., Kulski J.K., Inoko H.;  
 RT "Phylogenetic analysis of penguin(Spheniscidae) species based on  
 sequence variation in MHC class II genes.";  
 RL Immunogenetics 53:712-716(2001).  
 DR ENBL; AB043556; BAB86820.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0045012; F:MHC class II receptor activity; IEA.  
 DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.  
 DR GO; GO:0019886; P:antigen processing, exogenous antigen; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR000353; MHC\_II\_beta.  
 DR Pfam; PF00969; MHC\_II\_beta; 1.  
 DR ProDom; PD000328; MHC\_II\_beta; 1.  
 KW Glycoprotein; MHC II; Transmembrane.  
 FT NON\_TER 1 66  
 FT NON\_TER 66  
 SQ SEQUENCE 66 AA; 7839 MW; 841AD0C90029FDC7 CRC64;  
 Query Match 100.0%; Score 21; DB 7; Length 66;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YVAD 4  
 DB 29 YVAD 32

Db 29 YVAD 32

Search completed: May 24, 2004, 14:41:00  
Job time : 38.5 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 24, 2004, 14:36:17 ; Search time 51 Seconds  
(without alignments)  
22.161 Million cell updates/sec

Title: US-09-765-105A-2

Perfect score: 21

Sequence: 1 DEVD 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	4	2	AAW06250 ICE pepti
2	21	100.0	4	2	AAW76200 Mouse cas
3	21	100.0	4	2	AAW52756 Aminometh
4	21	100.0	4	2	AAW48940 Apopain (
5	21	100.0	4	2	AAW56305 Peptide c
6	21	100.0	4	2	AAW48948 Apopain (
7	21	100.0	4	2	AAW15622 Peptide u
8	21	100.0	4	2	AAW04114 Enzyme co
9	21	100.0	4	2	AAW68554 Apopain a
10	21	100.0	4	2	AAW24411 Caspase p
11	21	100.0	4	2	AAW99676 Caspase r
12	21	100.0	4	2	AAW94093 Protease
13	21	100.0	4	3	AAW78347 Caspase 1
14	21	100.0	4	3	AAW69646 Caspase 1
15	21	100.0	4	3	AAW99958 Tetrapapt
16	21	100.0	4	3	AAW22899 Caspase 3
17	21	100.0	4	3	AAW49940 Synthetic
18	21	100.0	4	3	AAW79040 Caspase 1
19	21	100.0	4	3	AAW88373 Peptide u
20	21	100.0	4	3	AAW83396 DEVD pept
21	21	100.0	4	3	AAW36851 Synthetic
22	21	100.0	4	3	AAW80786 Fluoropho
23	21	100.0	4	3	AAW17431 Caspase 3
24	21	100.0	4	3	AAW69866 PARP clea
25	21	100.0	4	3	AAW10870 Aminocoum

ALIGNMENTS

RESULT 1

AAW06250

ID AAW06250 standard; peptide; 4 AA.

XX AC AAW06250;

DT 03-MAR-1997 (first entry)

DE ICE peptide substrate.

XX Mch2; Ced-3/Ice; cysteine protease; apoptosis; autoimmune disease;

XX cancer; HIV; Alzheimer's disease; therapy.

OS Synthetic.

PN WO9636698-A1.

PD 21-NOV-1996.

PF 16-MAY-1996; 96WO-US007010.

PR 18-MAY-1995; 95US-00446925.

XX (UYJE-) UNIV JEFFERSON THOMAS.

PI Litwack G, Alnemri ES, Fernandez-Alnemri T;

DR WPI; 1997-012077/01.

XX New isolated apoptotic cysteine protease, Mch 2 - used to develop prods. for use as anti-apoptotic agents or as cytotoxic agents.

PS Disclosure; Page 28; 43pp; English.

XX A tetrapeptide (AAW06250) represents a site present in poly (ADP- ribose) that is cleaved by an interleukin-1 beta converting enzyme (ICE)-like protein during apoptosis. Another tetrapeptide (AAW06453) is the ICE cleavage site in pro-interleukin-1 beta. The 2 peptides were used to test the activity of human Cpp32, ICE and 2 isoforms, alpha (see also AAW06244) and beta (AAW06245), of novel human apoptotic cysteine protease Mch2. Enzymatic activities were studied in total bacterial extracts from cells expressing these enzymes as GST fusion proteins. Neither Mch2 alpha nor Mch2 beta was able to cleave the YVAD substrate. Mch2 alpha, but not Mch2 beta, cleaved the DEVD substrate, but was 150-fold less active than CPP32

XX Sequence 4 AA;

SQ

AAY67491 Caspase 3  
AAY81937 APF agonl  
AAY57561 Synthetic  
AAY87641 Caspase 3  
AAB26704 Caspase s  
AAY81392 Caspase s  
AAB21110 Synthetic  
AAY56897 Caspase i  
AAY79591 Caspase-3  
AAB28540 Caspase-3  
AAB21941 Control p  
AAB32120 Tetrapept  
AAB59582 Chromogen  
AAE11216 Caspase-3  
AAG62552 Cresyl vi  
AAG62560 Cresyl vi  
AAG62557 Cresyl vi  
AAG62546 Cresyl vi  
AAG67377 Peptide s  
AAG67378 Peptide s

Query Match 100.0%; Score 21; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
 ||||  
 Db 1 DEVD 4

RESULT 2  
 AAW76200  
 ID AAW76200 standard; protein; 4 AA.  
 AC AAW76200;  
 XX  
 XX  
 DT 26-NOV-1998 (first entry)  
 XX  
 XX Mouse caspase I peptide motif #2.  
 DE  
 XX Caspase; thymocyte; inhibitor; immature; treatment; cancer; autoreactive;  
 KW leukemia; melanoma; autoimmune disease; apoptosis; lymphocyte; T cell;  
 KW receptor; infection; inflammatory disease; neurodegenerative disorder.  
 XX  
 OS Mus sp.  
 XX  
 FN WO9836057-A1.  
 XX  
 XX 20-AUG-1998.  
 PD  
 XX 17-FEB-1998; 98WO-US003524.  
 PF  
 XX 18-FEB-1997; 97US-00802474.  
 PR 09-OCT-1997; 97US-00948124.  
 XX  
 XX (DAND) DANA FARBER CANCER INST INC.  
 PA (PROC-) PROCEPT INC.  
 XX  
 PI Reinherz E, Clayton L, Ocain TD, Patch RJ;  
 XX  
 DR WPI; 1998-520756/44.  
 XX  
 XX Identifying agents which inhibit or enhance caspase activity - and which  
 PT may be used, e.g., in treatment of cancer or autoimmune diseases.  
 XX  
 XX Disclosure; Page 8; 62pp; English.  
 PS  
 XX AAW76198-W76202 are peptides used in a method for identifying an agent  
 CC which inhibits a caspase expressed in immature thymocytes. Such agents  
 CC may be used in the treatment of cancers (such as leukemia or melanomas)  
 CC and autoimmune diseases. Inhibition of apoptosis can result in the  
 CC inhibition of lymphocyte down regulation, resulting in a T cell receptor  
 CC population with an increased proportion of autoreactive T cells, i.e., an  
 CC increased occurrence of T cells which have specificity for the host  
 CC animal's own cells (e.g. cancer cells). By the same token, increasing the  
 CC activity of the caspase enzyme enhances apoptosis of self-recognising T  
 CC cells, resulting in a decrease in the population of T cells which are  
 CC responsible for autoimmune disorders. The compounds may also be useful in  
 CC treating infections, inflammatory diseases and neurodegenerative  
 CC disorders  
 XX  
 XX Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
 ||||  
 Db 1 DEVD 4

RESULT 3  
 AAW52756

AAW52756 standard; peptide; 4 AA.  
 AC AAW52756;  
 XX  
 XX 02-MAR-1999 (first entry)  
 DT  
 XX  
 DE Aminomethylcoumarin-substituted tetrapeptide.  
 XX  
 KW Aminomethylcoumarin; fluorescent; interleukin; ICE; caspase;  
 KW positional scanning synthetic combinatorial library.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FT Modified-site 1 /note= "the N-terminal is acetylated"  
 FT Modified-site 4  
 FT Modified-site 4 /note= "the C-terminal is condensed onto 7-amino- 4-  
 FT methyl-coumarin via an amide linkage"  
 XX  
 PN GB2324529-A.  
 XX  
 PD 28-OCT-1998.  
 XX  
 XX 20-FEB-1998; 98GB-00003559.  
 PF  
 XX 21-FEB-1997; 97US-0038656P.  
 PR  
 XX (MERI ) MERCK & CO INC.  
 PA  
 XX Chapman KT, Nicholson D, Rano T, Thornberry N;  
 PI  
 XX WPI; 1998-523841/45.  
 DR  
 XX New tetrapeptide coumarin derivatives - useful in combinatorial libraries  
 PT to identify substrate specificity of cysteine or serine proteases e.g.  
 PT interleukin-1 converting enzyme.  
 XX  
 PS Claim 3; Page 42; 49pp; English.  
 XX  
 CC The peptide is a specifically claimed example of new aminomethyl-  
 CC coumarin-labelled tetrapeptides of formula Ac-Xaa-Xaa-Xaa-asp-AMC. The  
 CC tetrapeptides are used to generate a fluorescent positional scanning  
 CC synthetic combinatorial library for the investigation of the substrate  
 CC specificity of cysteine and serine proteases, e.g. in the analysis of  
 CC interleukin-1 beta converting enzyme substrate and other caspase  
 CC substrates, and to identify inhibitors which may mediate inflammations.  
 CC The library preferably comprises a mixture of at least 200 of the  
 CC tetrapeptides  
 XX  
 XX Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
 ||||  
 Db 1 DEVD 4

RESULT 4  
 AAW48940  
 ID AAW48940 standard; protein; 4 AA.  
 AC AAW48940;  
 XX  
 XX 26-OCT-1998 (first entry)  
 DT  
 XX Apopain (caspase-3) peptide substrate.  
 DE  
 XX Apopain; caspase-3; protease; SPA; tyrosine phosphatase;  
 KW scintillation proximity binding assay; diabetes; cancer;

KW 4-phosphono(difluoromethyl) phenylalanine group; osteoporosis.  
 OS Synthetic.  
 XX  
 PN JP10099075-A.  
 XX  
 PD 21-APR-1998.  
 XX  
 PF 30-SEP-1996; 96JP-00276813.  
 XX  
 PR 30-SEP-1996; 96JP-00276813.  
 XX  
 PA (SHIS ) SHISEIDO CO LTD.  
 XX  
 DR WPI; 1998-289868/26.  
 XX  
 PT Protein with interleukin-1-beta converting enzyme-like activity - useful  
 in investigation of substrate specificity in, e.g. Parkinson's disease.  
 XX  
 PS Disclosure; Page 2; 5pp; Japanese.  
 XX  
 CC The present sequence, N-acetyl-DEVD-methyl coumarinamide (MCA),  
 represents a sequence that is cleaved by a protein with interleukin-1-  
 beta converting enzyme (ICE)-like activity. The protein, which is  
 obtained from human keratinocytes, has a relative molecular weight of 80  
 kDa. The ICE protein is part of the cysteine protease family and is  
 useful for investigation of the mechanism of substrate specificity (e.g.  
 Alzheimer's disease, Parkinson's disease, autoimmune disease, lymphoma,  
 cancer and apoptosis)  
 XX  
 SQ Sequence 4 AA;  
 PS  
 CC  
 CC Variants of the apopain (caspase-3) peptide substrate can be used as  
 ligands for the binding assay used in the invention. The invention  
 provides a method for use in a scintillation proximity binding assay  
 (SPA) for proteases and phosphatases. The method involves using mutated  
 proteases and phosphatases whereby the catalytic cysteine residue of the  
 enzymes are replaced with a serine or alanine residue to correct the  
 problem of interference in SPA from extraneous oxidising and alkylating  
 agents. The mutation affects the catalytic properties of the enzyme but  
 does not affect their binding properties. The invention claims for new  
 ligands for use in SPA which have increased binding affinity for a  
 tyrosine phosphatase or cysteine protease. The ligands contain at least  
 two 4-phosphono(difluoromethyl) phenylalanine groups which increase  
 binding affinity of the ligand to its respective enzyme. The assay can be  
 used to determine the ability of new ligands and compound mixtures to  
 competitively bind with an enzyme. The method is claimed to allow a  
 better usage of SPA in the discovery of compounds for the treatment and  
 study of diseases, e.g. diabetes, cancer and osteoporosis  
 XX  
 SQ Sequence 4 AA;  
 PS  
 CC  
 CC Query Match 100.0%; Score 21; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DEVD 4  
 DB ||||  
 1 DEVD 4  
 RESULT 5  
 ID AAW56305 standard; peptide; 4 AA.  
 AC AAW56305;  
 XX  
 XX 22-JUL-1998 (first entry)  
 DE Peptide cleaved by interleukin-1-beta-converting enzyme-like protein.  
 XX  
 KW N-acetyl-DEVD-methyl coumarinamide; MCA;  
 interleukin-1- beta converting enzyme-like activity; ICE activity;  
 cysteine protease; investigation; substrate specificity.  
 XX

OS Synthetic.  
 XX  
 PN JP10099075-A.  
 XX  
 PD 21-APR-1998.  
 XX  
 PF 30-SEP-1996; 96JP-00276813.  
 XX  
 PR 30-SEP-1996; 96JP-00276813.  
 XX  
 PA (SHIS ) SHISEIDO CO LTD.  
 XX  
 DR WPI; 1998-289868/26.  
 XX  
 PT Protein with interleukin-1-beta converting enzyme-like activity - useful  
 in investigation of substrate specificity in, e.g. Parkinson's disease.  
 XX  
 PS Disclosure; Page 2; 5pp; Japanese.  
 XX  
 CC The present sequence, N-acetyl-DEVD-methyl coumarinamide (MCA),  
 represents a sequence that is cleaved by a protein with interleukin-1-  
 beta converting enzyme (ICE)-like activity. The protein, which is  
 obtained from human keratinocytes, has a relative molecular weight of 80  
 kDa. The ICE protein is part of the cysteine protease family and is  
 useful for investigation of the mechanism of substrate specificity (e.g.  
 Alzheimer's disease, Parkinson's disease, autoimmune disease, lymphoma,  
 cancer and apoptosis)  
 XX  
 SQ Sequence 4 AA;  
 PS  
 CC  
 CC Query Match 100.0%; Score 21; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DEVD 4  
 DB ||||  
 1 DEVD 4  
 RESULT 6  
 ID AAW48948 standard; protein; 4 AA.  
 AC AAW48948;  
 XX  
 XX 26-OCT-1998 (first entry)  
 DE Apopain (caspase-3) peptide substrate.  
 XX  
 KW Apopain; caspase-3; protease; SPA; tyrosine phosphatase;  
 scintillation proximity binding assay; diabetes; cancer;  
 4-phosphono(difluoromethyl) phenylalanine group; osteoporosis.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1 /note= "N-terminal acetyl"  
 FT Modified-site 4  
 FT Modified-site 4 /note= "Optional attachment to aldehydes or ketones"  
 XX  
 PN WO9820156-A1.  
 XX  
 PD 14-MAY-1998.  
 XX  
 PF 03-NOV-1997; 97WO-CA000825.  
 XX  
 PR 04-NOV-1996; 96US-0030408P.  
 XX  
 PA (MERI ) MERCK FROSST CANADA INC.  
 XX  
 KW Desmarais S, Friesen R, Gresser M, Kennedy B, Nicholson D;  
 Ramachandran C, Skorey K, Ford-Hutchinson A;



XX WPI; 1998-348103/30.  
 XX Enzyme binding assay for detection of useful compounds - uses mutant form  
 PT of wild-type enzyme, in which serine replaces cysteine at active site, to  
 PT reduce interference from oxidising/alkylating agents.  
 XX Example; Page 28; 63pp; English.  
 XX Variants of the apocain (caspase-3) peptide substrate can be used as  
 CC ligands for the binding assay used in the invention. The invention claims  
 CC for a method for use in a scintillation proximity binding assay (SPA) for  
 CC proteases and phosphatases. The method involves using mutated proteases  
 CC and phosphatases whereby the catalytic cysteine residue of the enzymes  
 CC are replaced with a serine or alanine residue to correct the problem of  
 CC interference in SPA from extraneous oxidising and alkylating agents. The  
 CC mutation affects the catalytic properties of the enzyme but does not  
 CC affect their binding properties. The invention provides new ligands for  
 CC use in SPA which have increased binding affinity for a tyrosine  
 CC phosphatase or cysteine protease. The ligands contain at least two 4-  
 CC phosphono(difluoromethyl) phenylalanine groups which increase binding  
 CC affinity of the ligand to its respective enzyme. The assay can be used to  
 CC determine the ability of new ligands and compound mixtures to  
 CC competitively bind with an enzyme. The method is claimed to allow a  
 CC better usage of SPA in the discovery of compounds for the treatment and  
 CC study of diseases, e.g. diabetes, cancer and osteoporosis  
 XX SQ Sequence 4 AA;  
 Query Match 100.0%; Score 21; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DEVD 4  
 DB ||||  
 1 DEVD 4  
 RESULT 7  
 AAY15622  
 ID AAY15622 standard; peptide; 4 AA.  
 AC AAY15622;  
 XX 27-JUL-1999 (first entry)  
 DT  
 DE Peptide used to make fluorescent reporter molecules.  
 XX Fluorogenic; fluorescent reporter molecule; enzyme substrate; apoptosis;  
 KW protease; peptidase; apoptosis cascade; cancer; chemotherapeutic agent;  
 KW cell death; viral protease activity.  
 XX Synthetic.  
 OS  
 XX WO9918856-A1.  
 PN  
 XX 22-APR-1999.  
 PD  
 XX 09-OCT-1998; 98WO-US021231.  
 PF  
 XX 10-OCT-1997; 97US-0061582P.  
 PR  
 XX 03-MAR-1998; 98US-00033661.  
 XX (CYTO-) CYTOVIA INC.  
 PA  
 XX Weber E, Cai SX, Keana JFW, Drewe JA, Zhang H;  
 PI  
 XX WPI; 1999-312448/26.  
 DR  
 XX New fluorogenic or fluorescent reporter molecules.  
 PT  
 XX Claim 3; Page 160; 202pp; English.  
 XX

CC AAY15618-Y15759 represent peptides used to make the fluorogenic or  
 CC fluorescent reporter molecules of the invention. These molecules contain  
 CC a peptide moiety (e.g. present sequence) which acts as a substrate for  
 CC enzymes involved in apoptosis or protease or peptidase enzymes. The  
 CC compounds can be used as fluorogenic or fluorescent substrates for  
 CC enzymes. Depending on the peptide moiety used, the fluorescent molecules  
 CC can be used for detecting or measuring the activity of an enzyme involved  
 CC in the apoptosis cascade in cells; to determine whether a test compound  
 CC has an effect on an enzyme involved in the apoptosis cascade in cells;  
 CC for determining the sensitivity of an animal with cancer to treatment  
 CC with chemotherapeutic agents or determining whether a test substance  
 CC inhibits, prevents, causes or enhances cell death of test cells; for  
 CC detecting or measuring the activity of a viral protease in cells; for  
 CC determining whether a test compound has an effect on the activity of a  
 CC viral protease in cells; and for measuring the activity or determining  
 CC whether a test substance has an effect on the activity of a protease or  
 CC peptidase in cells  
 XX SQ Sequence 4 AA;  
 Query Match 100.0%; Score 21; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DEVD 4  
 DB ||||  
 1 DEVD 4  
 RESULT 8  
 AAY04114  
 ID AAY04114 standard; peptide; 4 AA.  
 XX  
 AC AAY04114;  
 XX  
 DT 15-JUN-1999 (first entry)  
 DE Enzyme component #2 caspase recognition sequence.  
 XX  
 KW Cross-linked polypeptide assay; cross-linked enzyme component; cleavage;  
 KW HIV; protease cleavage site.  
 XX Synthetic.  
 OS  
 XX WO9906537-A1.  
 PN  
 XX 11-FEB-1999.  
 PD  
 XX 23-JUL-1998; 98WO-US015343.  
 PF  
 XX 30-JUL-1997; 97US-00902766.  
 PR  
 XX (BOE ) BOEHRINGER MANNHEIM CORP.  
 PA  
 XX Powell MJ, Khanna P, Eisenbeis SJ, Lingenfelter D, Tietze LF;  
 PI  
 XX Manning W;  
 PI  
 XX WPI; 1999-190002/16.  
 DR  
 XX New cross-linked enzyme components - which have inhibited ability to  
 PT complement with other enzyme components to form an active enzyme complex.  
 PT  
 XX Example 10; Page 34; 56pp; English.  
 PS  
 XX The present invention describes a cross-linked enzyme component (A),  
 CC which: (i) has an inserted enzyme recognition site (ERS) in a polypeptide  
 CC of the component; and (ii) has at least one covalent intrachain cross-  
 CC link between amino acid side chains of the polypeptide. The component  
 CC forms an enzymatically active complex with a second enzyme component,  
 CC upon cleavage of the ERS, but is inhibited from forming this complex,  
 CC prior to cleavage. The complex has enzymatic activity which is different  
 CC from that of beta-galactosidase. The component may be used for  
 CC measurement of substances in biological samples. It is especially useful

CC for measurement of enzymes (e.g. proteases, particularly viral,  
 CC phosphatases, glycosidase, amidase and esterase) in clinical samples, or  
 CC for measurement of target polynucleotides. Assay methods using the new  
 CC components exhibit extremely low inherent background signals, due to  
 CC reduction or inhibition of complementation of enzyme components prior to  
 CC cleavage. The present sequence represents a peptide from an example of  
 CC the present invention

XX  
 SQ Sequence 4 AA;  
 Query Match 100.0%; Score 21; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
 ||||  
 Db 1 DEVD 4

RESULT 9  
 AAW68554  
 ID AAW68554 standard; protein; 4 AA.

XX  
 AC AAW68554;  
 XX  
 DT 25-JAN-1999 (first entry)  
 XX  
 DE Apoptain aldehyde-inhibitor peptide L-761191.  
 XX  
 KW Inhibitor; apopain; binding site; crystal structure; primer; PCR;  
 KW amplification; Escherichia coli; apoptosis.  
 XX  
 OS Synthetic.

XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1  
 FT Modified-site 4 /notes "acylated N-terminus"  
 FT Modified-site 4 /notes "contains C-terminal aldehyde group replacing  
 FT Modified-site 4 carboxyl group"

XX US5834228-A.  
 XX  
 PD 10-NOV-1998.

XX 13-FEB-1997; 97US-00800007.

XX 13-FEB-1997; 97US-00800007.

XX (MERI ) MERCK & CO INC.

XX (MERI ) MERCK FROSST CANADA INC.

XX Thornberry NA, Gallant M, Fazil KM, Nicholson DW, Peterson EP;  
 PI Rasper DM, Labelle M, Vaillancourt JP, Rotonda J, Ruel R, Becker JW;  
 PI Gareau Y;

XX WPI; 1999-008706/01.

XX Identifying inhibitors of apopain by rational drug design - from ability  
 PT to bind to the enzyme's substrate binding domain, potentially useful for  
 PT inhibiting apoptosis, e.g. in treatment of acquired immune deficiency  
 PT syndrome, autoimmune disease, infections etc.

XX Claim 1; Col 29; 22pp; English.

XX The invention relates to the identification of inhibitors of apopain by  
 CC designing and synthesising a potential inhibitor that will form non-  
 CC covalent bonds with amino acids in the apopain substrate binding site  
 CC based upon the crystal structure co-ordinates of an apopain:acetyl-DEVD-  
 CC CHO complex, testing it for apopain inhibition. Production of apopain for  
 CC the binding studies comprises expression of the p17 and p12 subunits  
 CC separately. This sequence represents an aldehyde-inhibitor of apopain  
 CC designated L-761191. The apopain inhibitors are potentially useful for

CC inhibiting apoptosis  
 XX  
 SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
 ||||  
 Db 1 DEVD 4

RESULT 10  
 AAY24411  
 ID AAY24411 standard; peptide; 4 AA.

XX  
 AC AAY24411;  
 XX  
 DT 20-SEP-1999 (first entry)  
 XX  
 DE Caspase processing site peptide #2 in aldehyde form.  
 XX  
 KW Human; caspase; anti-apoptosis; processing site; aldehyde; apoptosis;  
 KW hepatitis; ischaemic cerebral disease; Alzheimer's disease; cancer;  
 KW diarrhoea; bone marrow toxicity.

XX Homo sapiens.  
 OS Synthetic.

XX JP11180891-A.

XX 06-JUL-1999.

XX 25-DEC-1997; 97JP-00356757.

XX 25-DEC-1997; 97JP-00356757.

XX (DAUC ) DAIICHI PHARM CO LTD.

XX WPI; 1999-439401/37.

XX New anti-apoptosis agents - useful for treating hepatitis, ischemic  
 PT cerebral diseases and Alzheimer's disease.

XX Claim 6; Page 6; 7pp; Japanese.

XX The present invention describes anti-apoptosis agent(s) containing human  
 CC caspase and/or inhibitor(s) of its inducer(s), (especially human caspase-  
 CC 1, human caspase-3 and/or a human caspase-3 inducer) comprising de-  
 CC processing the process of human caspase inhibitor into active type of  
 CC human caspase inducer. Also describes are anti-apoptosis agent(s)  
 CC containing a modified protein comprising amino acid sequence around the  
 CC processing site of caspase, especially aldehyde form of protein composed  
 CC of amino acids of Tyr-Val-Ala-Asp, Asp-Glu-Val-Asp, and Glu-Ser-Met-Asp,  
 CC especially Glu-Ser-Met-Asp, used for treatment of disease caused by  
 CC apoptosis including hepatitis, ischaemic cerebral diseases, Alzheimer's  
 CC disease, adverse reactions of bone marrow toxicity and diarrhoea due to  
 CC administration of anticancer agent, especially hepatitis. The agents(s)  
 CC are useful for treating disease caused by apoptosis e.g. ischaemic  
 CC cerebral diseases, Alzheimer's disease, adverse reactions of bone marrow  
 CC toxicity and diarrhoea due to administration of anticancer agent,  
 CC especially hepatitis

XX Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
 ||||  
 Db 1 DEVD 4



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Db      1 DEVD 4

RESULT 13
AAV78347
ID      AAY78347 standard; peptide; 4 AA.
XX
XX
AC      AAY78347;
XX
XX      05-MAY-2000 (first entry)
XX
XX      Caspase 1 peptide Dns-SS-DEVD-CHO.
DE
XX
KW      Caspase; protein array; screening; biomolecular activity; proteomic;
KW      drug development; biosensor; diagnosis.
XX
XX      Unidentified.
OS
XX      Key Location/Qualifiers
FH      Modified-site 1
FT      /note= "Asp is N-terminally modified to dansyl-SS-Asp"
FT      Modified-site 4
FT      /note= "Asp is C-terminally modified to Asp-CHO"
XX
XX      WO200004382-A1.
XX
XX      27-JAN-2000.
XX
XX      14-JUL-1999; 99WO-US015971.
XX
XX      14-JUL-1998; 98US-00115455.
XX      (ZYOM-) ZYOMYX INC.
PA
XX      Wagner P, Ault-Riche D, Nock S, Itin C;
PI      WPI; 2000-171289/15.
XX
XX
XX      New arrays for analyzing components of a fluid sample, useful for drug
XX      development, functional proteomics, clinical diagnostics and biosensors.
XX      Example 7; Page 55; 81pp; English.
XX
XX      The present invention describes an array (I) of proteins comprising a
XX      substrate, at least one organic thinfilm on some or all of the substrate
XX      surface, and patches arranged in discrete, known regions on portions of
XX      the substrate surface covered by organic thinfilm. Each of the patches
XX      comprises a protein immobilised on the underlying organic thinfilm. The
XX      arrays can be used for screening proteins for their ability to interact
XX      with a component of a sample. They can also be used for assaying for
XX      protein-protein binding interactions or analytes. They can be used for
XX      drug development, proteomics, clinical diagnostics and biosensors. The
XX      present sequence represents a peptide used in the exemplification of the
XX      present invention
XX
XX      Sequence 4 AA;
SQ

Query Match 100.0%; Score 21; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. NO. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DEVD 4
      ||||
Db      1 DEVD 4

RESULT 14
AAV69646
ID      AAY69646 standard; peptide; 4 AA.
XX
XX      AAY69646;
AC
XX
XX      08-MAY-2000 (first entry)
XX

```

ID AAY99958 standard; peptide; 4 AA.  
AC AAY99958;  
XX  
DT 27-OCT-2000 (first entry)  
XX  
DE Tetrapeptide aldehyde which is a potent inhibitor of caspase-3.  
XX  
KW Inhibitor; apoptosis; cardiac; cerebral ischemia; stroke;  
KW type I diabetes; immune deficiency syndrome; HIV; AIDS; cerebral;  
KW spinal cord trauma injury; alopecia; ageing; Parkinson's disease;  
KW Alzheimer's disease; Down's syndrome; spinal muscular atrophy;  
KW multiple sclerosis; neurodegenerative disorders; caspase;  
KW gamma-ketoacid tetrapeptide; cysteine proteases.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1  
FT /note= "N-terminal acetyl"  
FT Modified-site 4  
FT /note= "D(CHO)"  
XX  
PN WO200032620-A1.  
XX  
PD 08-JUN-2000.  
XX  
PF 30-NOV-1999; 99WO-CA001145.  
XX  
PR 02-DEC-1998; 98US-0110567P.  
XX  
PA (MERI ) MERCK FROSST CANADA & CO.  
XX  
PI Grimm EL, Renaud J, Aspiotis R, Bayly CI, Zamboni R, Black S;  
XX  
DR WPI; 2000-412282/35.  
XX  
PT New gamma-ketoacid tetrapeptide compounds having caspase-3 inhibiting  
PT activity, useful for treating e.g. Parkinson's disease, organ damage  
PT during transportation, alopecia and ageing.  
XX  
PS Disclosure; Page 4; 121pp; English.  
XX  
CC The present invention relates to gamma-ketoacid tetrapeptide compounds,  
CC which have been found to inhibit caspase-3. Inhibition of caspase  
CC activity is known to inhibit apoptosis. The present sequence is a  
CC tetrapeptide aldehyde which is a very potent inhibitor of caspase-3. This  
CC peptide was designed to mimic the caspase-3 recognition site (see  
CC AAY99957). Caspase-3 inhibitors may be used for treating cardiac and  
CC cerebral ischemia/reperfusion injury (e.g. stroke), type I diabetes,  
CC immune deficiency syndrome (e.g. HIV or AIDS), cerebral and spinal cord  
CC trauma injury, alopecia, ageing, Parkinson's disease, Alzheimer's  
CC disease, Down's syndrome, spinal muscular atrophy, multiple sclerosis and  
CC neurodegenerative disorders. They may also be used for treating other  
CC caspase-3 mediated diseases  
XX  
SQ Sequence 4 AA;  
  
Query Match 100.0%; Score 21; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.4e-06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 DEVD 4  
Db 1 DEVD 4  
  
Search completed: May 24, 2004, 14:38:16  
Job time : 52 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 24, 2004, 14:36:17 ; Search time 16.5 Seconds  
(without alignments)  
12.515 Million cell updates/sec

Title: US-09-765-105A-2

Perfect score: 21

Sequence: 1 DEVD 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*

1: /cgn2\_6/prodata/2/1aa/5A\_COMB.pep:\*

2: /cgn2\_6/prodata/2/1aa/5B\_COMB.pep:\*

3: /cgn2\_6/prodata/2/1aa/6A\_COMB.pep:\*

4: /cgn2\_6/prodata/2/1aa/6B\_COMB.pep:\*

5: /cgn2\_6/prodata/2/1aa/PCTUS\_COMB.pep:\*

6: /cgn2\_6/prodata/2/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	4	1	US-08-446-925-9
2	21	100.0	4	2	US-08-800-007A-10
3	21	100.0	4	2	US-09-146-331-9
4	21	100.0	4	2	US-08-915-414A-1
5	21	100.0	4	2	US-08-896-885-9
6	21	100.0	4	2	US-08-712-878-2
7	21	100.0	4	3	US-09-226-568-39
8	21	100.0	4	3	US-08-802-981-2
9	21	100.0	4	3	US-09-270-735-2
10	21	100.0	4	3	US-09-167-921-42
11	21	100.0	4	3	US-09-270-736-1
12	21	100.0	4	3	US-08-761-483-3
13	21	100.0	4	3	US-08-761-483-10
14	21	100.0	4	3	US-09-323-743-42
15	21	100.0	4	3	US-09-058-969-2
16	21	100.0	4	3	US-09-130-193-1
17	21	100.0	4	3	US-09-130-193-7
18	21	100.0	4	3	US-09-130-193-12
19	21	100.0	4	3	US-09-130-193-15
20	21	100.0	4	3	US-09-357-952-5
21	21	100.0	4	3	US-09-309-003-1
22	21	100.0	4	3	US/08/869
23	21	100.0	4	3	US-09-257-218-81
24	21	100.0	4	3	US-09-257-218-82
25	21	100.0	4	3	US-09-311-760-81
26	21	100.0	4	3	US-09-311-760-82
27	21	100.0	4	3	US-09-291-692-71

28 21 100.0 4 4 US-09-521-650-5 Sequence 5, Appl1  
29 21 100.0 4 4 US-09-188-888-5 Sequence 5, Appl1  
30 21 100.0 4 4 US-09-545-565-3 Sequence 3, Appl1  
31 21 100.0 4 4 US-09-375-256-9 Sequence 9, Appl1  
32 21 100.0 4 4 US-09-561-756-52 Sequence 52, Appl1  
33 21 100.0 4 4 US-09-237-721-52 Sequence 52, Appl1  
34 21 100.0 4 4 US-09-115-455-4 Sequence 4, Appl1  
35 21 100.0 4 4 US-09-376-156-9 Sequence 9, Appl1  
36 21 100.0 4 4 US-09-513-783A-60 Sequence 60, Appl1  
37 21 100.0 4 4 US-08-865-579-81 Sequence 81, Appl1  
38 21 100.0 4 4 US-08-865-579-82 Sequence 82, Appl1  
39 21 100.0 4 4 US-09-495-120-1 Sequence 1, Appl1  
40 21 100.0 4 4 US-09-353-215-4 Sequence 1, Appl1  
41 21 100.0 4 4 US-09-649-810B-1 Sequence 4, Appl1  
42 21 100.0 4 4 US-08-724-378D-17 Sequence 17, Appl1  
43 21 100.0 4 4 US-08-842-760A-3 Sequence 3, Appl1  
44 21 100.0 4 4 US-09-482-813-2 Sequence 2, Appl1  
45 21 100.0 4 4 US-09-300-374-1 Sequence 1, Appl1

#### ALIGNMENTS

RESULT 1  
US-08-446-925-9  
; Sequence 9, Application US/08446925  
; Patent No. 5672500  
; GENERAL INFORMATION:  
; APPLICANT: Litwack, Gerald  
; APPLICANT: Alnemri, Emad S.  
; TITLE OF INVENTION: MCH2, AN APOPTOTIC CYSTEINE  
; TITLE OF INVENTION: PROTEASE,  
; TITLE OF INVENTION: AND COMPOSITIONS FOR MAKING AND  
; TITLE OF INVENTION: METHODS  
; TITLE OF INVENTION: OF USING THE SAME  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &  
; ADDRESSEE: No. 5672500ris  
; STREET: One Liberty Place, 46th floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/446,925  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DeLuca, Mark  
; REGISTRATION NUMBER: 33,229  
; REFERENCE/DOCKET NUMBER: TJJ-1508  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-3100  
; TELEFAX: (215) 568-3439  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-446-925-9

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
11111  
Db 1 DEVD 4

RESULT 2  
US-08-800-007A-10  
; Sequence 10, Application US/08800007A  
; Patent No. 5834228  
; GENERAL INFORMATION:  
; APPLICANT: Becker, Joseph  
; APPLICANT: Nicholson, Donald  
; APPLICANT: Rotonda, Jennifer  
; APPLICANT: Thornberry, Nancy  
; APPLICANT: Fazil, Kimberly  
; APPLICANT: Gallant, Michel  
; APPLICANT: Gareau, Yves  
; APPLICANT: Labelle, Marc  
; APPLICANT: Peterson, Erin  
; APPLICANT: Rasper, Dita  
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF APOPAIN  
; TITLE OF INVENTION: AND USES THEREOF  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: JOSEPH A. COPPOLA - MERCK & CO., INC.  
; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000  
; CITY: RAHWAY  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/800,007A  
; FILING DATE: 13-FEB-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: COPPOLA, JOSEPH A  
; REGISTRATION NUMBER: 38,413  
; REFERENCE/DOCKET NUMBER: 19644  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 732-594-6734  
; TELEFAX: 732-594-4720  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-800-007A-10

Query Match 100.0%; Score 21; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
11111  
Db 1 DEVD 4

RESULT 3  
US-09-146-331-9  
; Sequence 9, Application US/09146331  
; Patent No. 5958720  
; GENERAL INFORMATION:

; APPLICANT: Litwack, Gerald  
; APPLICANT: Alnemri, Emad S.  
; APPLICANT: Fernandez-Alnemri, Teresa  
; TITLE OF INVENTION: Mch2. AN APOPTOTIC CYSTEINE  
; TITLE OF INVENTION: PROTEASE AND COMPOSITIONS FOR MAKING AND  
; TITLE OF INVENTION: METHODS OF USING THE SAME  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &  
; ADDRESSEE: No. 5958720ris  
; STREET: One Liberty Place, 46th floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/146,331  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/896,885  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Deluca, Mark  
; REGISTRATION NUMBER: 33,229  
; REFERENCE/DOCKET NUMBER: TJU-1508  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-3100  
; TELEFAX: (215) 568-3439  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-146-331-9

Query Match 100.0%; Score 21; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
11111  
Db 1 DEVD 4

RESULT 4  
US-08-915-414A-1  
; Sequence 1, Application US/08915414A  
; Patent No. 5976822  
; GENERAL INFORMATION:  
; APPLICANT: LANDRUM, ET AL.  
; TITLE OF INVENTION: METHOD AND REAGENT FOR MONITORING APOPTOSIS  
; TITLE OF INVENTION: AND DISTINGUISHING APOPTOSIS FROM NECROSIS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MITCHELL ALTER, COULTER INTERN. CORP.  
; STREET: 11800 SW 147 AVE.  
; CITY: MIAMI  
; STATE: FLORIDA  
; COUNTRY: USA  
; ZIP: 33196  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Microsoft Word 6.0/95  
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/915,414A  
FILING DATE: 20-AUG-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/444,051  
FILING DATE: 18-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: MITCHELL E. ALTER  
REGISTRATION NUMBER: 28,684  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (305) 380-3636  
TELEFAX: (305) 380-4566  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
US-08-915-414A-1

Query Match 100.0%; Score 21; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
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Db 1 DEVD 4

RESULT 5  
US-08-896-885-9  
Sequence 9, Application US/08896885  
Patent No. 5985640  
GENERAL INFORMATION:  
APPLICANT: Litwack, Gerald  
APPLICANT: Alnemri, Emad S.  
APPLICANT: Fernandez-Alnemri, Teresa  
TITLE OF INVENTION: Mch2, AN APOPTOTIC CYSTEINE  
PROTEASE, AND COMPOSITIONS FOR MAKING AND  
METHODS OF USING THE SAME  
TITLE OF INVENTION: METHODS OF USING THE SAME  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &  
ADDRESSEE: No. 5985640ris  
STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/896,885  
FILING DATE: 18-JUL-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/446,925  
FILING DATE: 18-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: TJU-1508  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-896-885-9  
Query Match 100.0%; Score 21; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DEVD 4  
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Db 1 DEVD 4

RESULT 6  
US-08-712-878-2  
Sequence 2, Application US/08712878  
Patent No. 5985863  
GENERAL INFORMATION:  
APPLICANT: Su, Michael  
APPLICANT: Gu, Yong  
APPLICANT: Livingston, David J.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DECREASING  
IGIF AND IFN-GAMMA PRODUCTION BY ADMINISTERING AN ICE  
INHIBITOR  
TITLE OF INVENTION: INHIBITOR  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr.  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/712,878  
FILING DATE: 12-SEP-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: VFI/96-05  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /note: "aspartic acid is  
OTHER INFORMATION: acetylated"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 4  
OTHER INFORMATION: /note: "aspartic acid carboxy  
terminus is reduced to an aldehyde"  
US-08-712-878-2

Query Match 100.0%; Score 21; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 1 DEVD 4  
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Db 1 DEVD 4

RESULT 7

US-09-226-568-39  
; Sequence 39, Application US/09226568  
; Patent No. 6001992  
; GENERAL INFORMATION:  
; APPLICANT: Ackermann, Elizabeth J.  
; APPLICANT: Bennett, C. Frank  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Marcuseon, Eric G.  
; TITLE OF INVENTION: Antisense Modulation of No. 6001992el Anti-apoptotic  
; FILE REFERENCE: bcl-2-Related Proteins  
; FILE REFERENCE: ISPH-0337  
; CURRENT FILING DATE: 1999-01-07  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 39  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-226-568-39

Query Match 100.0%; Score 21; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4  
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Db 1 DEVD 4

RESULT 8

US-08-802-981-2  
; Sequence 2, Application US/08802981  
; Patent No. 6037137  
; GENERAL INFORMATION:  
; APPLICANT: Komoriya, Akira  
; APPLICANT: Packard, Beverly S.  
; TITLE OF INVENTION: Compositions for the Detection of Enzyme  
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof  
; NUMBER OF SEQUENCES: 231  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/802,981  
; FILING DATE: 20-FEB-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hunter, Tom  
; REGISTRATION NUMBER: 38,498  
; REFERENCE/DOCKET NUMBER: 016865-000300US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-802-981-2

Query Match 100.0%; Score 21; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4  
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Db 1 DEVD 4

RESULT 9

US-09-270-735-2  
; Sequence 2, Application US/09270735  
; Patent No. 6135591  
; GENERAL INFORMATION:  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Drewe, John  
; APPLICANT: Wang, Yan  
; APPLICANT: Weber, Eckard  
; TITLE OF INVENTION: Dipeptide Caspase Inhibitors and the Use Thereof  
; FILE REFERENCE: 1735.0010001  
; CURRENT APPLICATION NUMBER: US/09/270,735  
; CURRENT FILING DATE: 1999-03-16  
; EARLIER APPLICATION NUMBER: 60/078,051  
; EARLIER FILING DATE: 1998-03-16  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: peptide  
US-09-270-735-2

Query Match 100.0%; Score 21; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4  
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|  
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Db 1 DEVD 4

RESULT 10

US-09-167-921-42  
; Sequence 42, Application US/09167921A  
; Patent No. 6172216  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, C. Frank  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Nickoloff, Brian J.  
; APPLICANT: Zhang, QingQing  
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression  
; FILE REFERENCE: ISPH-0324  
; CURRENT APPLICATION NUMBER: US/09/167,921A  
; CURRENT FILING DATE: 1998-10-07  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 42  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: caspase assay substrate

US-09-167-921-42

Query Match 100.0%; Score 21; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;

Qy 1 DEVD 4  
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Db 1 DEVD 4

RESULT 11

US-09-270-736-1  
; Sequence 1, Application US/09270736  
; Patent No. 6184210  
; GENERAL INFORMATION:  
; APPLICANT: Keana, John F. W.  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Guastella, John  
; APPLICANT: Yang, Wu  
; APPLICANT: Drewe, John A.  
; APPLICANT: Weber, Eckard  
; TITLE OF INVENTION: Dipeptide Apoptosis Inhibitors and the Use Thereof  
; FILE REFERENCE: 1735.0280002  
; CURRENT APPLICATION NUMBER: US/09/270,736  
; CURRENT FILING DATE: 1999-03-16  
; EARLIER APPLICATION NUMBER: US 09/168,945  
; EARLIER FILING DATE: 1998-10-09  
; EARLIER APPLICATION NUMBER: US 60/061,676  
; EARLIER FILING DATE: 1997-10-10  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-270-736-1

Query Match 100.0%; Score 21; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;

Qy 1 DEVD 4  
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Db 1 DEVD 4

RESULT 12

US-08-761-483-3  
; Sequence 3, Application US/08761483  
; Patent No. 6204261  
; GENERAL INFORMATION:  
; APPLICANT: Batchelor, Mark J  
; APPLICANT: Bebbington, David  
; APPLICANT: Bemis, Guy W  
; APPLICANT: Fridman, Wolf H  
; APPLICANT: Gillespie, Roger J  
; APPLICANT: Golec, Julian MC  
; APPLICANT: Gu, Yong  
; APPLICANT: Lauffer, David J  
; APPLICANT: Livingston, David J  
; APPLICANT: Matharu, Saroop S  
; TITLE OF INVENTION: INHIBITORS OF INTERLEUKIN-1 BETA  
; TITLE OF INVENTION: CONVERTING ENZYME  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York

COUNTRY: USA

ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/761,483  
FILING DATE: 06-DEC-1996  
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr, James F  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: VPI/36-01CIP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /note= "Aspartic acid is  
OTHER INFORMATION: acetylated"

FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 4  
OTHER INFORMATION: /note= "aspartic acid terminal acid  
OTHER INFORMATION: is reduced to an aldehyde"

US-08-761-483-3  
Query Match 100.0%; Score 21; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4  
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Db 1 DEVD 4

RESULT 13

US-08-761-483-10  
; Sequence 10, Application US/08761483  
; Patent No. 6204261  
; GENERAL INFORMATION:  
; APPLICANT: Batchelor, Mark J  
; APPLICANT: Bebbington, David  
; APPLICANT: Bemis, Guy W  
; APPLICANT: Fridman, Wolf H  
; APPLICANT: Gillespie, Roger J  
; APPLICANT: Golec, Julian MC  
; APPLICANT: Gu, Yong  
; APPLICANT: Lauffer, David J  
; APPLICANT: Livingston, David J  
; APPLICANT: Matharu, Saroop S  
; TITLE OF INVENTION: INHIBITORS OF INTERLEUKIN-1 BETA  
; TITLE OF INVENTION: CONVERTING ENZYME  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10020

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/761,483  
FILING DATE: 06-DEC-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr, James F  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: VPI/96-01CIP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 4  
OTHER INFORMATION: /note="aspartic acid is  
OTHER INFORMATION: derivatized with amino-4-methylcoumarin"  
US-08-761-483-10

Query Match 100.0%; Score 21; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4  
Db 1 DEVD 4

RESULT 14  
US-09-323-743-42  
Sequence 42, Application US/09323743  
Patent No. 6214986  
GENERAL INFORMATION:  
APPLICANT: Bennett, C. Frank  
APPLICANT: Dean, Nicholas M.  
APPLICANT: Monia, Brett P.  
APPLICANT: Nickoloff, Brian J.  
APPLICANT: Zhang, QingQing  
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression  
FILE REFERENCE: ISPH-0368  
CURRENT APPLICATION NUMBER: US/09/323,743  
CURRENT FILING DATE: 1999-06-01  
EARLIER APPLICATION NUMBER: 09/277,020  
EARLIER FILING DATE: 1998-03-26  
EARLIER APPLICATION NUMBER: 09/167,921  
EARLIER FILING DATE: 1998-10-07  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 42  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-09-323-743-42

Query Match 100.0%; Score 21; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4  
Db 1 DEVD 4  
RESULT 15  
US-09-058-969-2  
Sequence 2, Application US/09058969A  
Patent No. 6228603  
GENERAL INFORMATION:  
APPLICANT: Reed, John C.  
APPLICANT: Devereaux, Quinn  
APPLICANT: Salvesen, Guy S.  
APPLICANT: Takahashi, Ryosuke  
APPLICANT: Roy, Natalie  
TITLE OF INVENTION: Screening Assays For Agents That Alter Inhibitor of  
Apoptosis (IAP) Protein Regulation of Caspase Activity  
FILE REFERENCE: LJ 3080  
CURRENT APPLICATION NUMBER: US/09/058,969A  
CURRENT FILING DATE: 1998-04-10  
EARLIER APPLICATION NUMBER: 08/862,087  
EARLIER FILING DATE: 1997-05-22  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism: Consensus Sequence  
US-09-058-969-2

Query Match 100.0%; Score 21; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 DEVD 4

Search completed: May 24, 2004, 14:39:00  
Job time : 17.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 24, 2004, 14:39:37 ; Search time 38 Seconds  
(without alignments)  
29,360 Million cell updates/sec

Title: US-09-765-105A-2

Perfect score: 21  
Sequence: 1 DEVD 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1149313 seqs, 278921704 residues

Total number of hits satisfying chosen parameters: 1149313

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/pubpaa/ECT\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
  - 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
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  - 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
  - 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
  - 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
  - 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
  - 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
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  - 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
  - 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
  - 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	21	100.0	4	9	US-09-734-846-42
3	21	100.0	4	9	US-09-799-463-2
4	21	100.0	4	9	US-09-735-363A-85
5	21	100.0	4	9	US-09-799-994-2
6	21	100.0	4	9	US-09-352-768-71
7	21	100.0	4	9	US-09-858-754-11
8	21	100.0	4	9	US-09-587-417-3
9	21	100.0	4	9	US-09-737-255-1
10	21	100.0	4	9	US-09-920-332-1
11	21	100.0	4	9	US-09-845-028-8
12	21	100.0	4	9	US-09-954-697-52
13	21	100.0	4	9	US-09-347-387-5
14	21	100.0	4	10	US-09-161-172-2
15	21	100.0	4	10	US-09-866-512A-7

16	21	100.0	4	10	US-09-862-224-1	Sequence 1, Appli
17	21	100.0	4	12	US-10-227-012-8	Sequence 8, Appli
18	21	100.0	4	12	US-10-182-975-3	Sequence 3, Appli
19	21	100.0	4	12	US-10-452-184-1	Sequence 1, Appli
20	21	100.0	4	12	US-10-668-955-71	Sequence 71, Appl
21	21	100.0	4	12	US-09-746-731-81	Sequence 81, Appl
22	21	100.0	4	12	US-09-746-731-82	Sequence 82, Appl
23	21	100.0	4	12	US-09-765-105-2	Sequence 2, Appli
24	21	100.0	4	12	US-09-780-142-3	Sequence 3, Appli
25	21	100.0	4	12	US-09-863-649-2	Sequence 2, Appli
26	21	100.0	4	12	US-09-270-983-9	Sequence 9, Appli
27	21	100.0	4	12	US-09-819-266-1	Sequence 1, Appli
28	21	100.0	4	12	US-10-099-408A-3	Sequence 3, Appli
29	21	100.0	4	12	US-10-146-138A-1	Sequence 1, Appli
30	21	100.0	4	12	US-10-151-119B-1	Sequence 1, Appli
31	21	100.0	4	12	US-10-168-447-5	Sequence 5, Appli
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33	21	100.0	4	13	US-10-103-448-6	Sequence 6, Appli
34	21	100.0	4	13	US-10-059-749-81	Sequence 81, Appl
35	21	100.0	4	13	US-10-059-749-82	Sequence 82, Appl
36	21	100.0	4	13	US-10-108-929-6	Sequence 6, Appli
37	21	100.0	4	14	US-10-141-769-1	Sequence 1, Appli
38	21	100.0	4	14	US-10-171-077-9	Sequence 9, Appli
39	21	100.0	4	14	US-10-171-417-7	Sequence 7, Appli
40	21	100.0	4	14	US-10-164-705-1	Sequence 1, Appli
41	21	100.0	4	14	US-10-158-827-1	Sequence 1, Appli
42	21	100.0	4	14	US-10-105-779-1	Sequence 1, Appli
43	21	100.0	4	14	US-10-066-805A-1	Sequence 1, Appli
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ALIGNMENTS

RESULT 1  
US-09-045-620-4  
; Sequence 4, Application US/09045620  
; Patent No. US20010006793A1  
; GENERAL INFORMATION:  
; APPLICANT: BJORNSTI, Mary-Ann  
; APPLICANT: KANG, David  
; APPLICANT: KANG, Jason  
; TITLE OF INVENTION: MODULATORS OF EUKARYOTIC CASPASES  
; FILE REFERENCE: 209855.0037/27US  
; CURRENT APPLICATION NUMBER: US/09/045,620  
; CURRENT FILING DATE: 2000-03-20  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Fluorometric  
; OTHER INFORMATION: caspase-specific peptide  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (4)  
; OTHER INFORMATION: aminomethyl coumarin linked with residue 4  
US-09-045-620-4

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Db 1 DEVD 4

RESULT 2  
US-09-734-846-42

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; Sequence 42, Application US/09734846
; Patent No. US20010007025A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Nickoloff, Brian J.
; APPLICANT: Zhang, QingGang
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
; FILE REFERENCE: ISPH-0528
; CURRENT APPLICATION NUMBER: US/09/734,846
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 09/277,020
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 09/167,921
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 09/323,743
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-734-846-42

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Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
Db 1 DEVD 4
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RESULT 3
US-09-799-463-2
; Sequence 2, Application US/09799463
; Patent No. US20010018195A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Devereaux, Quinn
; APPLICANT: Salvesen, Guy S.
; APPLICANT: Takahashi, Ryosuke
; APPLICANT: Roy, Natalie
; TITLE OF INVENTION: Screening Assays For Agents That Alter Inhibitor of
; TITLE OF INVENTION: Apoptosis (IAP) Protein Regulation of Caspase Activity
; FILE REFERENCE: LJ 3080
; CURRENT APPLICATION NUMBER: US/09/799,463
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 09/058,969
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 08/862,087
; PRIOR FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:Consensus Sequence
; US-09-799-463-2

Query Match 100.0%; Score 21; DB 9; Length 4;
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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
Db 1 DEVD 4
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RESULT 4
US-09-735-363A-85
; Sequence 85, Application US/09735363A
; Patent No. US20010041681A1
; GENERAL INFORMATION:
; APPLICANT: Filion, Mario
; APPLICANT: Phillip, Nigel
; TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
; FILE REFERENCE: 02811-0181
; CURRENT APPLICATION NUMBER: US/09/735,363A
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/170,325
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 60/228,925
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 85
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; US-09-735-363A-85

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Qy 1 DEVD 4
Db 1 DEVD 4
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RESULT 5
US-09-799-994-2
; Sequence 2, Application US/09799994
; Patent No. US20020009757A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Devereaux, Quinn
; APPLICANT: Salvesen, Guy S.
; APPLICANT: Takahashi, Ryosuke
; APPLICANT: Roy, Natalie
; TITLE OF INVENTION: Screening Assays For Agents That Alter Inhibitor of
; TITLE OF INVENTION: Apoptosis (IAP) Protein Regulation of Caspase Activity
; FILE REFERENCE: LJ 3080
; CURRENT APPLICATION NUMBER: US/09/799,994
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 09/058,969
; PRIOR FILING DATE: 1998-04-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:Consensus Sequence
; US-09-799-994-2

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Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
Db 1 DEVD 4

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Matches	4	Conservative	0	Mismatches	0	Indels	0
QY	1	DEVD	4				
DB	1	DEVD	4				
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QY	1	DEVD	4				
DB	1	DEVD	4				
US-09-858-754-11							
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Matches	4	Conservative	0	Mismatches	0	Indels	0
QY	1	DEVD	4				
DB	1	DEVD	4				
US-09-858-754-11							
Query Match	100.0%	Score	21	DB	9	Length	4
Best Local Similarity	100.0%	Pred. No.	1e+06				
Matches	4	Conservative	0	Mismatches	0	Indels	0
QY	1	DEVD	4				
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US-09-858-754-11							
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Matches	4	Conservative	0	Mismatches	0	Indels	0
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DB	1	DEVD	4				
US-09-858-754-11							
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Best Local Similarity	100.0%	Pred. No.	1e+06				
Matches	4	Conservative	0	Mismatches	0	Indels	0
QY	1	DEVD	4				
DB	1	DEVD	4				
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Query Match	100.0%	Score	21	DB	9	Length	4
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Matches	4	Conservative	0	Mismatches	0	Indels	0
QY	1	DEVD	4				
DB	1	DEVD	4				
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Query Match	100.0%	Score	21	DB	9	Length	4
Best Local Similarity	100.0%	Pred. No.	1e+06				
Matches	4	Conservative	0	Mismatches	0	Indels	0
QY	1	DEVD	4				
DB	1	DEVD	4				
US-09-858-754-11							
Query Match	100.0%	Score	21	DB	9	Length	4
Best Local Similarity	100.0%	Pred. No.	1e+06				
Matches	4	Conservative	0	Mismatches	0	Indels	0
QY	1	DEVD	4				
DB	1	DEVD	4				
US-09-858-754-11							
Query Match	100.0%	Score	21	DB	9	Length	4
Best Local Similarity	100.0%	Pred. No.	1e+06				
Matches	4	Conservative	0	Mismatches	0	Indels	0
QY	1	DEVD	4				
DB	1	DEVD					

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Qy      1 DEVD 4
Db      1 DEVD 4

RESULT 10
US-09-920-332-1
; Sequence 1, Application US/09920332
; Patent No. US2002007673A1
; GENERAL INFORMATION:
; APPLICANT: Kasibhatla, Shailaja
; APPLICANT: Green, Douglas R.
; APPLICANT: Tseng, Ben
; TITLE OF INVENTION: Method of Identifying Immunosuppressive Agents
; FILE REFERENCE: 1735.0470001/RWE/ALS
; CURRENT APPLICATION NUMBER: US/09/920,332
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/222,897
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fluorogenic substrate
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLTATION
US-09-920-332-1
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Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DEVD 4
Db      1 DEVD 4

RESULT 11
US-09-845-028-8
; Sequence 8, Application US/09845028
; Patent No. US20020081705A1
; GENERAL INFORMATION:
; APPLICANT: Mankovich, John
; TITLE OF INVENTION: HUMAN CASPASE-14 COMPOSITIONS
; FILE REFERENCE: BSI-111
; CURRENT APPLICATION NUMBER: US/09/845,028
; CURRENT FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/199,962
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-028-8
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Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DEVD 4
Db      1 DEVD 4

RESULT 12
US-09-954-697-52
; Sequence 52, Application US/09954697
; Patent No. US20020106631A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954,697
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 52
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-954-697-52
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Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DEVD 4
Db      1 DEVD 4

RESULT 13
US-09-947-387-5
; Sequence 5, Application US/09947387
; Patent No. US20020150895A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. US20020150895A1el Fluorogenic or Fluorescent Reporter Molecu
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290005
; CURRENT APPLICATION NUMBER: US/09/947,387
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/061,582
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/145,746
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: US 09/168,888
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-947-387-5
Query Match      100.0%; Score 21; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14
US-09-161-172-2
; Sequence 2, Application US/09161172
; Publication No. US2003004476A1
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Job time : 38 secs

GENERAL INFORMATION:  
APPLICANT: Dykens, James A.  
APPLICANT: Miller, Scott W.  
APPLICANT: Ghosh, Soumitra S.  
APPLICANT: Davis, Robert E.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING  
TITLE OF INVENTION: AGENTS THAT ALTER MITOCHONDRIAL PERMEABILITY  
TITLE OF INVENTION: TRANSITION PORES  
FILE REFERENCE: 660088.418  
CURRENT APPLICATION NUMBER: US/09/161,172  
CURRENT FILING DATE: 1998-09-25  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: caspase-3 specific fluorogenic peptide substrate  
US-09-161-172-2

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Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15  
US-09-866-512A-7  
Sequence 7, Application US/09866512A  
Publication No. US2003053954A1  
GENERAL INFORMATION:  
APPLICANT: Meade, Thomas J  
TITLE OF INVENTION: Agents  
TITLE OF INVENTION: Magnetic Resonance Imaging Agents for the Detection of Physiological  
FILE REFERENCE: A-58634-7  
CURRENT APPLICATION NUMBER: US/09/866,512A  
CURRENT FILING DATE: 2001-05-24  
PRIOR APPLICATION NUMBER: US 60/287,619  
PRIOR FILING DATE: 2001-05-26  
PRIOR APPLICATION NUMBER: US 08/460,511  
PRIOR FILING DATE: 1995-06-02  
PRIOR APPLICATION NUMBER: US 08/486,968  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: US 08/971,855  
PRIOR FILING DATE: 1997-11-17  
PRIOR APPLICATION NUMBER: US 09/134,072  
PRIOR FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 09/866,512  
PRIOR FILING DATE: 2001-05-24  
PRIOR APPLICATION NUMBER: US 09/405,046  
PRIOR FILING DATE: 1999-09-27  
PRIOR APPLICATION NUMBER: US 60/063,328  
PRIOR FILING DATE: 1997-10-27  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn version 3.1  
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LENGTH: 4  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: could be from any mammal.  
US-09-866-512A-7

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Best Local Similarity 100.0%; Pred. No. 1e+06;  
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Oy 1 DEVD 4  
Db 1 DEVD 4

Agg  
Res



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

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Title: US-09-765-105A-2

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37	21	100.0	4	14	US-09-023-130-11	Sequence 11, Appli
38	21	100.0	4	14	US-09-026-716-15	Sequence 15, Appli
39	21	100.0	4	14	US-09-045-620-4	Sequence 4, Appli
40	21	100.0	4	14	US-09-099-463-27	Sequence 27, Appli
41	21	100.0	4	14	US-09-099-463A-27	Sequence 2, Appli
42	21	100.0	4	15	US-09-161-172-2	Sequence 2, Appli
43	21	100.0	4	16	US-09-242-286A-1	Sequence 1, Appli
44	21	100.0	4	16	US-09-270-983-9	Sequence 9, Appli
45	21	100.0	4	16	US-09-296-682-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
PCT-US00-02329-1  
; Sequence 1, Application PC/TUS0002329  
; GENERAL INFORMATION:  
; APPLICANT: Cytovia, Inc.  
; TITLE OF INVENTION: Methods of Identifying Potentially Therapeutically Effective Antineoplastic Agents with Viable Cultured Cells Having an Intact Cell Membrane and Product by  
; TITLE OF INVENTION: Cells Having an Intact Cell Membrane and Product by  
; TITLE OF INVENTION: Same  
; FILE REFERENCE: 1735.032PC02  
; CURRENT APPLICATION NUMBER: PCT/US00/02329  
; CURRENT FILING DATE: 2000-02-01  
; EARLIER APPLICATION NUMBER: 60/118,102  
; EARLIER FILING DATE: 1999-02-01  
; EARLIER APPLICATION NUMBER: 09/454,595  
; EARLIER FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: Patent Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 4  
; TYPE: PPT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
PCT-US00-02329-1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
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DB 1 DEVD 4

RESULT 2  
PCT-US00-02332-1  
; Sequence 1, Application PC/TUS0002332  
; GENERAL INFORMATION:  
; APPLICANT: CYTOVIA, INC.  
; APPLICANT: CAI, SUI XIONG  
; APPLICANT: ZHANG, HAN-ZHONG  
; APPLICANT: WANG, YAN  
; APPLICANT: TSENG, BEN  
; APPLICANT: KASIBHATLA, SHAILAIA  
; APPLICANT: DREWE, JOHN A.  
; TITLE OF INVENTION: GAMBOGIC ACID, ANALOGS AND DERIVATIVES AS ACTIVATORS OF  
; FILE REFERENCE: 1735.032PC03  
; CURRENT APPLICATION NUMBER: PCT/US00/02332  
; CURRENT FILING DATE: 2000-02-01  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
PCT-US00-02332-1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
|||  
DB 1 DEVD 4

RESULT 3  
PCT-US00-09319-3  
; Sequence 3, Application PC/TUS0009319  
; GENERAL INFORMATION:  
; APPLICANT: Cytovia, Inc.  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Weber, Eckard  
; APPLICANT: Wang, Yan  
; APPLICANT: Mills, Gordon B.  
; APPLICANT: Green, Douglas R.  
; TITLE OF INVENTION: Caspase Inhibitors and the Use Thereof  
; FILE REFERENCE: 1735.035PC02  
; CURRENT APPLICATION NUMBER: PCT/US00/09319  
; CURRENT FILING DATE: 2000-04-07  
; EARLIER APPLICATION NUMBER: US 60/128,545  
; EARLIER FILING DATE: 1998-04-09  
; EARLIER APPLICATION NUMBER: US 60/158,370  
; EARLIER FILING DATE: 1999-10-12  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Caspase  
; OTHER INFORMATION: inhibitor

; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: caspase 3  
; OTHER INFORMATION: substrate  
PCT-US00-09319-3

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
|||  
DB 1 DEVD 4

RESULT 4  
PCT-US00-14451-42  
; Sequence 42, Application PC/TUS0014451  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, C. Frank  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Nickoloff, Brian J.  
; APPLICANT: Zhang, QingQing  
; APPLICANT: ISIS PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression  
; FILE REFERENCE: ISPH-0460  
; CURRENT APPLICATION NUMBER: PCT/US00/14451  
; CURRENT FILING DATE: 2000-05-25  
; PRIOR APPLICATION NUMBER: 09/323,743  
; PRIOR FILING DATE: 1999-06-02  
; PRIOR APPLICATION NUMBER: 09/167,921  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 09/277,020  
; PRIOR FILING DATE: 1999-03-26  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 42  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
PCT-US00-14451-42

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
|||  
DB 1 DEVD 4

RESULT 5  
PCT-US01-04137-1  
; Sequence 1, Application PC/TUS0104137  
; GENERAL INFORMATION:  
; APPLICANT: ALEXION PHARMACEUTICALS, INC.  
; APPLICANT: Fodor, William L.  
; TITLE OF INVENTION: MIXTURES OF CASPASE INHIBITORS AND COMPLEMENT  
; FILE REFERENCE: 1087-15PCT  
; CURRENT APPLICATION NUMBER: PCT/US01/04137  
; CURRENT FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Caspase  
; OTHER INFORMATION: inhibitor

PCT-US01-04137-1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
|  
|  
|  
|  
Db 1 DEVD 4

RESULT 6

PCT-US01-48256-1

; Sequence 1, Application PC/TUS0148256  
; GENERAL INFORMATION:  
; APPLICANT: Regents of the University of Michigan  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING  
; TITLE OF INVENTION: PROTEOLYTIC ACTIVITY  
; FILE REFERENCE: 11203-003W01  
; CURRENT APPLICATION NUMBER: PCT/US01/48256  
; PRIOR FILING DATE: 2001-12-13  
; PRIOR APPLICATION NUMBER: 09/737,255  
; PRIOR FILING DATE: 2000-12-13  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Mus musculus

PCT-US01-48256-1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
|  
|  
|  
|  
Db 1 DEVD 4

RESULT 7

PCT-US02-04060-52

; Sequence 52, Application PC/TUS0204060  
; GENERAL INFORMATION:  
; APPLICANT: Massachusetts Institute of Technology, et al.  
; TITLE OF INVENTION: Peptides that Inhibit Poly-Glutamine Aggregation  
; FILE REFERENCE: M0656/7062W0 (GRV)  
; CURRENT APPLICATION NUMBER: PCT/US02/04060  
; CURRENT FILING DATE: 2002-02-11  
; PRIOR APPLICATION NUMBER: US 60/267,898  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/334,891  
; PRIOR FILING DATE: 2001-11-15  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 52  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Caspase Inhibitor

PCT-US02-04060-52

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
|  
|  
|  
|  
Db 1 DEVD 4

RESULT 8

PCT-US01-48256-1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
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|  
|  
|  
Db 1 DEVD 4

RESULT 9

PCT-US02-14722-1

; Sequence 1, Application PC/TUS0214722  
; GENERAL INFORMATION:  
; APPLICANT: Cytovia, Inc.  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Kasibhatla, Shailaja  
; APPLICANT: Drewe, John  
; APPLICANT: Reddy, P. Sanjeeva  
; APPLICANT: Zhang, Han-Zhong  
; TITLE OF INVENTION: Substituted N'-(Arylcabonyl)-Benzhydrazides,  
; TITLE OF INVENTION: N'-(Arylcabonyl)-Benzylidene-hydrazides And Analogs as Activators  
; TITLE OF INVENTION: Caspases and Inducers of Apoptosis And The Use Thereof  
; FILE REFERENCE: 1735.056PC01  
; CURRENT APPLICATION NUMBER: PCT/US02/14722  
; CURRENT FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: US 60/289,803  
; PRIOR FILING DATE: 2001-05-10  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fluorogenic substrate

PCT-US02-14722-1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
|  
|  
|  
|  
Db 1 DEVD 4

RESULT 10

PCT-US02-15398-1

; Sequence 1, Application PC/TUS0215398  
; GENERAL INFORMATION:  
; APPLICANT: CYTOVIA, INC.  
; APPLICANT: CAI, SUI XIONG

APPLICANT: JUAN, FDU M

APPLICANT: YUAN, PAU M

Job time : 176 secs

; TITLE OF INVENTION: Analogs as Activators of Caspases and Inducers of Apoptosis and  
; FILE REFERENCE: 1735.057PC01  
; CURRENT APPLICATION NUMBER: PCT/US02/17486  
; CURRENT FILING DATE: 2002-06-04  
; PRIOR APPLICATION NUMBER: US 60/295,007  
; PRIOR FILING DATE: 2001-04-06  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: fluorogenic substrate  
; NAME/KEY: MOD RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (4)..(4)  
; OTHER INFORMATION:  
; PCT-US02-17486-1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
|||  
Db 1 DEVD 4

RESULT 15  
PCT-US02-17892-1  
; Sequence 1, Application PC/TUS0217892  
; GENERAL INFORMATION:  
; APPLICANT: Cytovia, Inc.  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Zhang, Han-Zhong  
; APPLICANT: Drewe, John A.  
; APPLICANT: Reddy, P. Sanjeeva  
; APPLICANT: Kasibhatla, Shailaja  
; APPLICANT: Roemerle, Jared Daniel  
; APPLICANT: Ollis, Kristin P.  
; TITLE OF INVENTION: Substituted 3-Aryl-5-aryl-[1,2,4]-oxadiazoles and  
; TITLE OF INVENTION: Analogs as Activators of Caspases and Inducers of  
; TITLE OF INVENTION: Apoptosis and the Use Thereof  
; FILE REFERENCE: 1735.064PC01  
; CURRENT APPLICATION NUMBER: PCT/US02/17892  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: US 60/296,479  
; PRIOR FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fluorogenic substrate  
; PCT-US02-17892-1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 5.5e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
|||  
Db 1 DEVD 4

Search completed: May 24, 2004, 14:47:42

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 24, 2004, 14:39:07 ; Search time 13.5 seconds  
(without alignments)  
10.992 Million cell updates/sec

Title: US-09-765-105A-2

Perfect score: 21

Sequence: 1 DEVD 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 251736 seqs, 37097828 residues

Total number of hits satisfying chosen parameters: 251736

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents AA New.\*

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- 2: /cgn2\_6/prodata/1/paa/US06\_NEW\_COMB.pep.\*
- 3: /cgn2\_6/prodata/1/paa/US07\_NEW\_COMB.pep.\*
- 4: /cgn2\_6/prodata/1/paa/US08\_NEW\_COMB.pep.\*
- 5: /cgn2\_6/prodata/1/paa/US09\_NEW\_COMB.pep.\*
- 6: /cgn2\_6/prodata/1/paa/US10\_NEW\_COMB.pep.\*
- 7: /cgn2\_6/prodata/1/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	4	1	PCT-US03-20668A-1
2	21	100.0	4	1	PCT-US04-11915-41
3	21	100.0	4	1	PCT-US04-11916-23
4	21	100.0	4	6	US-10-768-976-64
5	21	100.0	4	6	US-10-630-926-14
6	21	100.0	4	6	US-10-826-905-43
7	21	100.0	4	6	US-10-626-258-22
8	21	100.0	4	6	US-10-471-720-1
9	21	100.0	4	6	US-10-030-378-1
10	21	100.0	4	6	US-10-263-330A-43
11	21	100.0	4	6	US-10-146-136-1
12	21	100.0	4	6	US-10-626-905A-43
13	21	100.0	4	6	US-10-826-893-1
14	21	100.0	4	6	US-10-826-909-41
15	21	100.0	4	6	US-10-826-923-23
16	21	100.0	4	6	US-10-829-381-5
17	21	100.0	4	6	US-10-844-470-39
18	21	100.0	4	7	US-60-549-602-4
19	21	100.0	5	1	PCT-US04-04752-15
20	21	100.0	5	1	PCT-US04-04752-19
21	21	100.0	5	6	US-10-684-346-41
22	21	100.0	5	6	US-10-684-346-42
23	21	100.0	5	6	US-10-829-381-76
24	21	100.0	7	1	PCT-US04-11915-42
25	21	100.0	7	1	PCT-US04-11915-44
26	21	100.0	7	1	PCT-US04-11916-24

27	21	100.0	7	1	PCT-US04-11916-26	Sequence 26, Appl
28	21	100.0	7	5	US-09-394-019B-196	Sequence 196, App
29	21	100.0	7	5	US-09-394-019B-198	Sequence 198, App
30	21	100.0	7	5	US-09-394-019B-208	Sequence 208, App
31	21	100.0	7	5	US-09-394-019B-193	Sequence 193, App
32	21	100.0	7	5	US-09-394-019B-195	Sequence 195, App
33	21	100.0	7	5	US-09-394-019B-205	Sequence 205, App
34	21	100.0	7	5	US-09-394-019C-196	Sequence 196, App
35	21	100.0	7	5	US-09-394-019C-198	Sequence 198, App
36	21	100.0	7	5	US-09-394-019C-208	Sequence 208, App
37	21	100.0	7	6	US-10-826-909-42	Sequence 42, Appl
38	21	100.0	7	6	US-10-826-909-44	Sequence 44, Appl
39	21	100.0	7	6	US-10-826-923-24	Sequence 24, Appl
40	21	100.0	7	6	US-10-826-923-26	Sequence 26, Appl
41	21	100.0	7	6	US-10-466-552A-1	Sequence 1, Appli
42	21	100.0	8	5	US-09-394-019B-189	Sequence 189, App
43	21	100.0	8	5	US-09-394-019B-197	Sequence 197, App
44	21	100.0	8	5	US-09-394-019B-186	Sequence 186, App
45	21	100.0	8	5	US-09-394-019B-194	Sequence 194, App

ALIGNMENTS

RESULT 1  
PCT-US03-20668A-1  
; Sequence 1, Application PC/TUS0320668A  
; GENERAL INFORMATION:  
; APPLICANT: CVTOVIA, INC.  
; APPLICANT: CAI, SUI XIONG  
; APPLICANT: TSENG, BEN  
; APPLICANT: ZHANG, HAN-ZHONG  
; APPLICANT: KASIBHATLA, SHAILAJA  
; APPLICANT: OLLIS, KRISTIN P.  
; APPLICANT: SIRISOVA, NILANTHA SUDATH  
; APPLICANT: DREWE, JOHN A.  
; TITLE OF INVENTION: Derivatives of Gambogic Acid And Analogs As Activators of  
; TITLE OF INVENTION: Caspases and Inducers of Apoptosis  
; FILE REFERENCE: 1735.078PC02  
; CURRENT APPLICATION NUMBER: PCT/US03/20668A  
; CURRENT FILING DATE: 2003-07-01  
; PRIOR APPLICATION NUMBER: 60/392,358  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/413,649  
; PRIOR FILING DATE: 2002-09-26  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: N-terminal acetyl  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (4)..(4)  
; OTHER INFORMATION: C-terminal N'-ethoxycarbonyl-Rhodamine 110  
PCT-US03-20668A-1

Query Match 100.0%; Score 21; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4

Db 1 DEVD 4

RESULT 2  
PCT-US04-11915-41  
; Sequence 41, Application PC/TUS0411915

```

; GENERAL INFORMATION:
; APPLICANT: Kasibhatla, Shailaja
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Tseng, Ben
; APPLICANT: Jessen, Katayoun Alavi
; APPLICANT: English, Nicole Marion
; APPLICANT: Maliartchouk, Serguei
; APPLICANT: Jiang, Songchun
; APPLICANT: Sirisoma, Nilantha Sudath
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Kuemmerle, Jared
; APPLICANT: Cytovia, Inc.
; TITLE OF INVENTION: Methods of Treating Diseases Responsive to Induction of Apoptosis
; FILE REFERENCE: 1735.084PC02
; CURRENT APPLICATION NUMBER: PCT/US04/11915
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/484,750
; PRIOR FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: US 60/463,649
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: US 60/532,665
; PRIOR FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: US 60/463,662
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: US 60/484,749
; PRIOR FILING DATE: 2003-07-07
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
PCT-US04-11915-41

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
Db 1 DEVD 4

RESULT 3
PCT-US04-11916-23
; Sequence 23, Application PC/TUS0411916
; GENERAL INFORMATION:
; APPLICANT: Kasibhatla, Shailaja
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Tseng, Ben
; APPLICANT: Jessen, Katayoun Alavi
; APPLICANT: Maliartchouk, Serguei
; APPLICANT: English, Nicole Marion
; APPLICANT: Kuemmerle, Jared
; APPLICANT: Kemnitzner, William E.
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Kuemmerle, Jared
; APPLICANT: Cytovia, Inc.
; TITLE OF INVENTION: Methods of Treating Diseases Responsive to Induction of Apoptosis
; FILE REFERENCE: 1735.087PC01
; CURRENT APPLICATION NUMBER: PCT/US04/11916
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: 60/463,687
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT

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; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
PCT-US04-11916-23

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
Db 1 DEVD 4

RESULT 4
US-10-768-976-64
; Sequence 64, Application US/10768976
; GENERAL INFORMATION:
; APPLICANT: Wood, Keith V.
; APPLICANT: Lee, Georgyi V.
; APPLICANT: Bulleit, Robert F.
; APPLICANT: Klauber, Dieter
; APPLICANT: McDougall, Mark
; APPLICANT: Zimprich, Chad
; APPLICANT: Promega Corporation
; TITLE OF INVENTION: Covalent Tethering of Functional Groups to Proteins
; FILE REFERENCE: 341.020J51
; CURRENT APPLICATION NUMBER: US/10/768,976
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: US 60/444,094
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 60/474,659
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A synthetic peptide
US-10-768-976-64

Query Match 100.0%; Score 21; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4
Db 1 DEVD 4

RESULT 5
US-10-630-926-14
; Sequence 14, Application US/10630926
; GENERAL INFORMATION:
; APPLICANT: Riccardi, Carlo
; TITLE OF INVENTION: INTRACELLULAR MODULATORS OF APOPTIC CELL
; DEATH PATHWAYS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEWMARK, P.L.L.C.
; STREET: 624 Ninth Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/10/630,926  
FILING DATE: 31-Jul-2003  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/403,861A  
FILING DATE: 11-Feb-2000  
APPLICATION NUMBER: PCT/EP98/02490  
FILING DATE: 27-Apr-1998  
APPLICATION NUMBER: EP 97107033.9  
FILING DATE: 28-Apr-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: YUN, Allen C.  
REGISTRATION NUMBER: 37,971  
REFERENCE/DOCKET NUMBER: RICCARDI=1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
OTHER INFORMATION: /note= "the N-terminus is modified by an acetyl group; the C-terminus is modified with a-(4-methyl-coumaryl-7-amide)"  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-10-630-926-14

Query Match 100.0%; Score 21; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
Db 1 DEVD 4

RESULT 6  
US-10-626-905-43  
GENERAL INFORMATION:  
APPLICANT: FRANZOSO, GUIDO  
APPLICANT: DESMAELE, ENRICO  
APPLICANT: ZAZZERONI, FRANCESCA  
APPLICANT: PAPA, SALVATORE  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING APOPTOSIS  
FILE REFERENCE: 21459-94575  
CURRENT FILING DATE: 2003-07-25  
PRIOR APPLICATION NUMBER: PCT/US02/31548  
PRIOR FILING DATE: 2002-10-02  
PRIOR APPLICATION NUMBER: 10/263,330  
PRIOR FILING DATE: 2002-10-02  
PRIOR APPLICATION NUMBER: 60/328,811  
PRIOR FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: 60/326,492  
PRIOR FILING DATE: 2001-10-02  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: PatentIn ver. 3.2  
SEQ ID NO 43  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-626-905-43

Query Match 100.0%; Score 21; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
Db 1 DEVD 4  
RESULT 7  
US-10-626-258-22  
GENERAL INFORMATION:  
APPLICANT: Snavelly, Marshall  
APPLICANT: Kliounsky, Lana  
TITLE OF INVENTION: Enhanced Solubility of Recombinant Proteins  
FILE REFERENCE: A-725  
CURRENT APPLICATION NUMBER: US/10/626,258  
CURRENT FILING DATE: 2003-07-23  
PRIOR APPLICATION NUMBER: US/09/715,521C  
PRIOR FILING DATE: 2000-11-17  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 22  
LENGTH: 4  
TYPE: PRT  
ORGANISM: caspase 3 protease  
US-10-626-258-22

Query Match 100.0%; Score 21; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
Db 1 DEVD 4

RESULT 8  
US-10-471-720-1  
GENERAL INFORMATION:  
APPLICANT: Cai, Sui Xiong  
APPLICANT: Reddy, P. Sanjeeva  
APPLICANT: Drewe, John A.  
APPLICANT: Nguyen, Bao Ngoc  
APPLICANT: Kasibhatla, Shailaja  
TITLE OF INVENTION: Multifluoro-substituted Chalcones and Analogs as Activators of Apoptosis and Inducers of Apoptosis and the Use Thereof  
FILE REFERENCE: 1735.0540001  
CURRENT APPLICATION NUMBER: US/10/471,720  
CURRENT FILING DATE: 2003-09-15  
PRIOR APPLICATION NUMBER: PCT/US02/07569  
PRIOR FILING DATE: 2002-03-14  
PRIOR APPLICATION NUMBER: US 60/275,473  
PRIOR FILING DATE: 2001-03-14  
NUMBER OF SEQ ID NOS: 1  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Fluorogenic substrate  
US-10-471-720-1

Query Match 100.0%; Score 21; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
Db 1 DEVD 4

RESULT 9  
US-10-030-378-1



THE UNIVERSITY OF CHICAGO

; APPLICANT: KEMNITZER, WILLIAM

```
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Kasibhatla, Shailaja
; APPLICANT: Drewe, John
; APPLICANT: Reddy, P. Sanjeeva
; APPLICANT: Zhang, Han-zhong
; TITLE OF INVENTION: Substituted N'-(Arylcabonyl)-Benzhydrazides,
; TITLE OF INVENTION: N'-(Arylcabonyl)-Benzylidene-hydrazides And Analogs as Activators
; TITLE OF INVENTION: Caspases and Inducers of Apoptosis And The Use Thereof
; FILE REFERENCE: 1735.0360002
; CURRENT APPLICATION NUMBER: US/10/816,893
; CURRENT FILING DATE: 2004-04-05
; PRIOR APPLICATION NUMBER: US 10/141,769
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/289,803
; PRIOR FILING DATE: 2001-05-10
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fluorogenic substrate
; US-10-816-893-1

Query Match      100.0%; Score 21; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DEVD 4
      ||||
DB      1 DEVD 4

RESULT 14
US-10-826-909-41
; Sequence 41, Application US/10826909
; GENERAL INFORMATION:
; APPLICANT: Kasibhatla, Shailaja
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Tseng, Ben
; APPLICANT: Jessen, Katayoun Alavi
; APPLICANT: English, Nicole Marion
; APPLICANT: Maliartchouk, Serguei
; APPLICANT: Jiang, Songchun
; APPLICANT: Sirisoma, Nilantha Sudath
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Kuemmerle, Jared
; TITLE OF INVENTION: Methods of Treating Diseases Responsive to Induction of Apoptosis
; FILE REFERENCE: 1735.0340002
; CURRENT APPLICATION NUMBER: US/10/826,909
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: US 60/484,750
; PRIOR FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: US 60/463,649
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: US 60/532,665
; PRIOR FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: US 60/463,662
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: US 60/484,749
; PRIOR FILING DATE: 2003-07-07
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; US-10-826-909-41
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Query Match      100.0%; Score 21; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DEVD 4
      ||||
DB      1 DEVD 4

RESULT 15
US-10-826-923-23
; Sequence 23, Application US/10826923
; GENERAL INFORMATION:
; APPLICANT: Kasibhatla, Shailaja
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Tseng, Ben
; APPLICANT: Jessen, Katayoun Alavi
; APPLICANT: Maliartchouk, Serguei
; APPLICANT: English, Nicole Marion
; APPLICANT: Kuemmerle, Jared
; APPLICANT: Kennitzer, William E.
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Kuemmerle, Jared
; TITLE OF INVENTION: Methods of Treating Diseases Responsive to Induction of Apoptosis
; FILE REFERENCE: 1735.0870001
; CURRENT APPLICATION NUMBER: US/10/826,923
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: 60/463,687
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; US-10-826-923-23

Query Match      100.0%; Score 21; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DEVD 4
      ||||
DB      1 DEVD 4

Search completed: May 24, 2004, 14:48:20
Job time : 13.5 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 24, 2004, 14:36:18 ; Search time 13.5 Seconds  
(without alignments)

28,501 Million cell updates/sec

Title: US-09-765-105A-2

Perfect score: 21

Sequence: 1 DEVD 4

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	21	100.0	16	2	PL0137	protein kinase, 80
2	21	100.0	18	2	B34473	calcium-binding pr
3	21	100.0	44	2	B43714	hydroxymethylgluta
4	21	100.0	45	2	D95155	hypothetical prote
5	21	100.0	49	2	T21746	hypothetical prote
6	21	100.0	58	2	PQ0129	34.5K linker prote
7	21	100.0	60	2	C69169	hypothetical prote
8	21	100.0	67	2	T17388	vrl1 protein - Dic
9	21	100.0	68	2	B71880	4-oxalocrotonate t
10	21	100.0	68	2	D64635	4-oxalocrotonate t
11	21	100.0	69	2	H81078	4-oxalocrotonate t
12	21	100.0	74	2	S82829	hypothetical prote
13	21	100.0	75	2	F64032	hypothetical prote
14	21	100.0	76	2	D91267	hypothetical prote
15	21	100.0	76	2	A86108	hypothetical prote
16	21	100.0	76	2	S56355	hypothetical 8.6K
17	21	100.0	82	2	A43337	sm region ORF1 pr
18	21	100.0	86	2	E70966	probable phage pro
19	21	100.0	97	2	E64509	hypothetical prote
20	21	100.0	98	1	W7WL11	E7 protein - human
21	21	100.0	98	1	W7WL6	E7 protein - human
22	21	100.0	98	1	W7WLC1	E7 protein - pygmy
23	21	100.0	99	2	E95237	preprotein translo
24	21	100.0	99	2	F98101	conserved hypothet
25	21	100.0	101	1	W7WL13	E7 protein - human
26	21	100.0	101	1	W7WL51	E7 protein - human
27	21	100.0	101	2	B86645	Glu-tRNA amidotran
28	21	100.0	103	2	F97138	hypothetical prote
29	21	100.0	104	2	A83871	hypothetical prote

30 21 100.0 105 2 F71348 probable DNA-bind  
31 21 100.0 105 2 S06985 probable nitrogen  
32 21 100.0 105 2 S36580 E7 protein - human  
33 21 100.0 105 2 S36528 E7 protein - human  
34 21 100.0 105 2 S36504 E7 protein - human  
35 21 100.0 107 2 G72868 hypothetical prote  
36 21 100.0 109 2 AD3626 hypothetical prote  
37 21 100.0 110 2 H72774 hypothetical prote  
38 21 100.0 110 2 S74013 hypothetical prote  
39 21 100.0 112 2 H69372 hypothetical prote  
40 21 100.0 112 2 F69320 conserved hypothet  
41 21 100.0 113 1 W7WLR1 E7 protein - thesu  
42 21 100.0 113 2 T13627 hypothetical prote  
43 21 100.0 118 2 D84918 hypothetical prote  
44 21 100.0 119 2 S17123 phage shock protei  
45 21 100.0 119 2 C90864 phage shock protei

#### ALIGNMENTS

##### RESULT 1

PL0137

protein kinase, 80K - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 18-Jun-1993

C:Accession: PL0137

R:Decheret, J.; Weber, M.; Weber-Schaeuffelen, M.; Wollny, E.

J. Neurochem. 53, 1268-1275, 1989

A:Title: Isolation and partial characterization of an 80,000-dalton protein kinase fr

A:Reference number: PL0137; MUID:89361455; PMID:2769266

A:Accession: PL0137

A:Molecule type: protein

A:Residues: 1-16 <DEC>

C:Comment: This protein has a novel serine/threonine-specific protein kinase activity.

Query Match 100.0%; Score 21; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 54;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4

DB 2 DEVD 5

##### RESULT 2

B34473

calcium-binding protein 4 - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 15-Jun-1990 #sequence\_revision 15-Jun-1990 #text\_change 31-Oct-1997

C:Accession: B34473

R:Van, P.N.; Peter, F.; Soeling, H.D.

J. Biol. Chem. 264, 17494-17501, 1989

A:Title: Four intracisternal calcium-binding glycoproteins from rat liver microsomes

A:Reference number: B34473; MUID:90008920; PMID:2793869

A:Accession: B34473

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-18 <VAN>

C:Superfamily: heat shock protein 90

C:Keywords: calcium binding

Query Match

Best Local Similarity 100.0%; Score 21; DB 2; Length 18;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4

DB 2 DEVD 5

##### RESULT 3

B43714  
 hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) - Pseudomonas sp. (fragment)  
 C:Species: Pseudomonas sp.  
 C>Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 26-May-2000  
 C/Accession: B43714  
 R:Anderson, D.H.; Rodwell, V.W.  
 J. Bacteriol. 171, 6468-6472, 1989  
 A:Title: Nucleotide sequence and expression in *Escherichia coli* of the 3-hydroxy-3-methylglutaryl-CoA reductase (NADPH)  
 A:Reference number: A43714; MUID:90078086; PMID:2687236  
 A/Accession: B43714  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-44 <AND>  
 A/Cross-references: GB:M31807; NID:G151370; PIDN:AAA25894.1; PID:G151371  
 C/Superfamily: Methanococcus jannaschii hydroxymethylglutaryl-CoA reductase (NADPH)  
 C/Keywords: coenzyme A; oxidoreductase

Query Match 100.0%; Score 21; DB 2; Length 44;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
 ||||  
 Db 14 DEVD 17

RESULT 4  
 D95155  
 hypothetical protein SPI339 [imported] - Streptococcus pneumoniae (strain TIGR4)  
 C:Species: Streptococcus pneumoniae  
 C>Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 03-Aug-2001  
 C/Accession: D95155  
 R:Tetterton, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidson, J.D.; Umayam, L.A.; White, C.; Salzberg, S.L.; Lewis, M.R.; Kadane, D.; Holtzapfel, T.; Hickey, E.K.; Holt, I.E.  
 Science 293, 498-506, 2001  
 A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A.  
 A:Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.  
 A:Reference number: A95000; MUID:21357209; PMID:11463916  
 A/Accession: D95155  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-45 <KUR>  
 A/Cross-references: GB:AE005672; PIDN:AAK75437.1; PID:G14972822; GSPDB:GN00164; TIGR:SP4  
 A/Experimental source: strain TIGR4  
 C/Genetics:  
 A/Gene: SPI339

Query Match 100.0%; Score 21; DB 2; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
 ||||  
 Db 19 DEVD 22

RESULT 5  
 T21746  
 hypothetical protein F35C12.1 - *Caenorhabditis elegans*  
 C:Species: *Caenorhabditis elegans*  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C/Accession: T21746  
 R:Baynes, C.  
 submitted to the EMBL Data Library, October 1996  
 A:Reference number: Z19468  
 A/Accession: T21746  
 A/Status: preliminary; translated from GB/EMBL/DDBJ  
 A/Molecule type: DNA  
 A/Residues: 1-49 <WIL>  
 A/Cross-references: EMBL:Z81075; PIDN:CAB03046.1; GSPDB:GN00019; CESP:F35C12.1  
 A/Experimental source: clone F35C12  
 C/Genetics:

A/Gene: CESP:F35C12.1  
 A/Map position: 1  
 A/Introns: 15/2

Query Match 100.0%; Score 21; DB 2; Length 49;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
 ||||  
 Db 33 DEVD 36

RESULT 6  
 PQ0129  
 34.5K linker protein - *Fischerella* sp. (fragment)  
 C:Species: *Fischerella* sp.  
 C>Date: 15-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 11-Jan-2000  
 C/Accession: PQ0129  
 R:Eberlein, M.; Kufer, W.  
 Gene 94, 133-136, 1990  
 A:Title: Genes encoding both subunits of phycoerythrocyanin, a light-harvesting biliprotein  
 A:Reference number: JQ0763; MUID:91033055; PMID:2121619  
 A/Accession: PQ0129  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-58 <EBE>  
 A/Cross-references: GB:M34254  
 C/Superfamily: phycoerythrin linker protein cpcH3

Query Match 100.0%; Score 21; DB 2; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
 ||||  
 Db 13 DEVD 16

RESULT 7  
 C69169  
 hypothetical protein MTH525 - *Methanobacterium thermoautotrophicum* (strain Delta H)  
 C:Species: *Methanobacterium thermoautotrophicum*  
 C>Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 22-Oct-1999  
 C/Accession: C69169  
 R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qi, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. K.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
 J. Bacteriol. 179, 7135-7155, 1997  
 A:Title: Complete genome sequence of *Methanobacterium thermoautotrophicum* Delta H: func  
 A:Reference number: A69000; MUID:98037514; PMID:9371463  
 A/Accession: C69169  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-60 <MTH>  
 A/Cross-references: GB:AE000835; GB:AE000666; NID:G2621586; PIDN:AAB85031.1; PID:G26215  
 A/Experimental source: strain Delta H  
 C/Genetics:  
 A/Gene: MTH525

Query Match 100.0%; Score 21; DB 2; Length 60;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
 ||||  
 Db 22 DEVD 25

RESULT 8  
 T17388  
 vrr1 protein - *Dichelobacter nodosus*  
 C:Species: *Dichelobacter nodosus*

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C;Accession: T17388  
R;Billington, S.J.; Huggins, A.S.; Johansen, P.A.; Crellin, P.K.; Chung, J.K.; Katz, M.  
Infect. Immun. 67, 1277-1286, 1999  
A;Title: Complete nucleotide sequence of the 27-kilobase virulence related locus (vrl) of  
A;Reference number: Z18734; MUID:99150261; PMID:10024571  
A;Accession: T17388  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-67 <BIL>  
A;Cross-references: EMBL:U20246; NID:G3493323; PID:G3482870; PIDN:AAC33397.1  
A;Experimental source: strain A198

Query Match 100.0%; Score 21; DB 2; Length 67;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

QY 1 DEVD 4  
|||  
45 DEVD 48

Db

RESULT 9  
B71880  
4-oxalocrotonate tautomerase (EC 5.3.2.-) jhp0858 [similarity] - Helicobacter pylori (st  
C;Species: Helicobacter pylori  
A;Variety: strain J99  
C;Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 17-Mar-2000  
C;Accession: B71880  
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;  
Ives, C.; Gibson, R.; Merberg, D.; Malle, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;  
Nature 397, 176-180, 1999  
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path  
A;Reference number: A71800; MUID:99120557; PMID:9923682  
A;Accession: B71880  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-68 <ARN>  
A;Cross-references: GB:AE001515; GB:AE001439; NID:G4155425; PIDN:AD06434.1; PID:G415542  
A;Experimental source: strain J99  
C;Genetics:  
A;Gene: jhp0858  
C;Superfamily: 4-oxalocrotonate tautomerase  
C;Keywords: aromatic hydrocarbon catabolism; intramolecular oxidoreductase; isomerase  
F;2-68/Product: 4-oxalocrotonate tautomerase #status predicted <MAT>  
F;2/Active site: Pro #status predicted

Query Match 100.0%; Score 21; DB 2; Length 68;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

QY 1 DEVD 4  
|||  
47 DEVD 50

Db

RESULT 10  
D64635  
4-oxalocrotonate tautomerase (EC 5.3.2.-) HP0924 [similarity] - Helicobacter pylori (str  
C;Species: Helicobacter pylori  
C;Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 17-Mar-2000  
C;Accession: D64635  
R;Tombs, J.F.; White, O.; Karlavags, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.  
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khairak, H.G.; Glodek, A.; McKenna  
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.  
Nature 388, 539-547, 1997  
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.  
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
A;Reference number: A64520; MUID:97394467; PMID:9252185  
A;Accession: D64635  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-68 <TOM>

A;Cross-references: GB:AE000602; GB:AE000511; NID:G2314060; PIDN:AD07977.1; PID:G2314  
C;Superfamily: 4-oxalocrotonate tautomerase  
C;Keywords: aromatic hydrocarbon catabolism; intramolecular oxidoreductase; isomerase  
F;2-66/Product: 4-oxalocrotonate tautomerase #status predicted <MAT>  
F;2/Active site: Pro #status predicted

Query Match 100.0%; Score 21; DB 2; Length 68;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

QY 1 DEVD 4  
|||  
47 DEVD 50

Db

RESULT 11  
H81078  
4-oxalocrotonate tautomerase (EC 5.3.2.-) NMB1474 [similarity] - Neisseria meningitidis  
C;Species: Neisseria meningitidis  
C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 02-Feb-2001  
C;Accession: H81078; H81863  
R;Hickley, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, C.  
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.F.  
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.  
Science 287, 1809-1815, 2000  
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;  
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A;Reference number: A81000; MUID:20175755; PMID:10710307  
A;Accession: H81078  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-69 <FET>  
A;Cross-references: GB:AE002497; GB:AE002098; NID:G7226712; PIDN:AAF41831.1; PID:G7226  
A;Experimental source: serogroup B, strain MC58  
R;Parthill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mc  
Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandrea  
Nature 404, 502-506, 2000  
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
A;Reference number: A81775; MUID:2022556; PMID:10761919  
A;Accession: H81863  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-69 <PAR>  
A;Cross-references: GB:AL162756; GB:AL157959; NID:G7380091; PIDN:CAE84913.1; PID:G7380  
A;Experimental source: serogroup A, strain Z2491  
C;Genetics:  
A;Gene: NMB1474; NMB1685  
C;Superfamily: 4-oxalocrotonate tautomerase  
C;Keywords: aromatic hydrocarbon catabolism; intramolecular oxidoreductase; isomerase  
F;2-69/Product: 4-oxalocrotonate tautomerase #status predicted <MAT>  
F;2/Active site: Pro #status predicted

Query Match 100.0%; Score 21; DB 2; Length 69;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

QY 1 DEVD 4  
|||  
47 DEVD 50

Db

RESULT 12  
E82829  
hypothetical protein XF0242 [imported] - Xylella fastidiosa (strain 9a5c)  
C;Species: Xylella fastidiosa  
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C;Accession: E82829  
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq  
Nature 406, 151-157, 2000  
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A;Reference number: A82515; MUID:20365717; PMID:10910347  
A;Note: for a complete list of authors see reference number A59328 below  
A;Accession: E82829

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-74 <SIN>
A;Cross-references: GB:AE003878; GB:AE003849; NID:g9105052; PIDN:AAF83055.1; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RMD 0509952
C;Genetics:
A;Gene: ECs5108

Query Match      100.0%; Score 21; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DEVD 4
      ||||
Db      52 DEVD 55

RESULT 15
A86108
hypothetical protein yjdi [imported] - Escherichia coli (strain O157:H7, substrain EDL5
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: A86108
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A86108
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-76 <STO>
A;Cross-references: GB:AE005174; NID:g12519102; PIDN:AA059325.1; GSPDB:GN00145; UNGPF:Z
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: yjdi

Query Match      100.0%; Score 21; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DEVD 4
      ||||
Db      52 DEVD 55

Search completed: May 24, 2004, 14:41:40
Job time : 14.5 secs

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-74 <SIN>
A;Cross-references: GB:AE003878; GB:AE003849; NID:g9105052; PIDN:AAF83055.1; GSPDB:GN00154
A;Experimental source: strain 9a5C
C;Genetics:
A;Gene: ECs5108

Query Match      100.0%; Score 21; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DEVD 4
      ||||
Db      64 DEVD 67

RESULT 13
F64032
hypothetical protein H11497 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C;Accession: F64032
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: F64032
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-75 <TIGR>
A;Cross-references: GB:U32826; GB:L42023; NID:g1574322; PIDN:AAC23137.1; PID:g1574327; T

Query Match      100.0%; Score 21; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DEVD 4
      ||||
Db      31 DEVD 34

RESULT 14
D91267
hypothetical protein ECs5108 [imported] - Escherichia coli (strain O157:H7, substrain R
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: D91267
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A;Reference number: A95629; MUID:21156231; PMID:11258796
A;Accession: D91267
A;Status: preliminary
A;Molecule type: DNA
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 24, 2004, 14:36:17 ; Search time 10.5 Seconds  
(without alignments)  
19.836 Million cell updates/sec

Title: US-09-765-105A-2

Perfect score: 21  
Sequence: 1 DEVD 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	21	100.0	20	1 FIBB_SHEEP	P14470 ovic aries
2	21	100.0	21	1 FIBB_ODOHE	P14476 odocoileus
3	21	100.0	60	1 YC60_BRAJA	Q89u29 bradyrhizob
4	21	100.0	63	1 MIP_BOTAS	P81C77 bothrops as
5	21	100.0	67	1 Y858_HELPF	Q92ks7 helicobacte
6	21	100.0	67	1 Y924_HELPF	O25581 helicobacte
7	21	100.0	75	1 YE97_HAEIN	P44221 haemophilus
8	21	100.0	76	1 YJDI_ECOLI	P39273 escherichia
9	21	100.0	77	1 MP5A_MBPS	P43174 ambrosia ps
10	21	100.0	88	1 EF1B_THEAC	Q9hkl1 thermoplasm
11	21	100.0	95	1 LSM2_HUMAN	Q9y333 homo sapien
12	21	100.0	97	1 VE7_HPV44	Q80914 human papil
13	21	100.0	97	1 VE7_HPV55	Q80935 human papil
14	21	100.0	97	1 YG75_METJA	Q59073 methanococ
15	21	100.0	98	1 VE7_HPV11	P04020 human papil
16	21	100.0	98	1 VE7_HPV6A	Q84292 human papil
17	21	100.0	98	1 VE7_HPV6B	P06464 human papil
18	21	100.0	98	1 VE7_PCPV1	Q02272 pygmy chimp
19	21	100.0	101	1 GATC_LACLA	Q9CJ44 lactococcus
20	21	100.0	101	1 VE7_HPV13	Q02271 human papil
21	21	100.0	101	1 VE7_HPV51	P26558 human papil
22	21	100.0	105	1 DBH_TREPA	O83278 treponema p
23	21	100.0	105	1 GLMT_METTL	P35771 methanococ
24	21	100.0	105	1 VE7_HPV30	P36826 human papil
25	21	100.0	105	1 VE7_HPV53	P36832 human papil
26	21	100.0	105	1 VE7_HPV56	P36833 human papil
27	21	100.0	113	1 CYAY_RALSO	Q8XV54 ralsonia s
28	21	100.0	113	1 VE7_RHPV1	P22161 rhesus papil
29	21	100.0	119	1 PSPC_ECOLI	P23855 escherichia
30	21	100.0	129	1 YSXI_CAEEL	Q10020 caenorhabdi
31	21	100.0	133	1 ATPB_MYCCE	P47638 mycoplasma
32	21	100.0	135	1 RS6E_HALMA	P21509 halocaula
33	21	100.0	138	1 YFFO_ECOLI	P76546 escherichia

34 21 100.0 140 1 BSR\_BACCE P33967 bacillus ce  
35 21 100.0 147 1 CALM\_FRAGS Q39752 fagus sylv  
36 21 100.0 148 1 CALM\_EMENI P19533 emericella  
37 21 100.0 148 1 CALM\_MAGGR Q9uWf0 magnaporthe  
38 21 100.0 148 1 CALM\_NEUCR Q02052 neurospora  
39 21 100.0 148 1 CALM\_PARTE P07463 paramecium  
40 21 100.0 151 1 DKSA\_ECOLI P18274 escherichia  
41 21 100.0 151 1 DKSA\_SALTY Q9ziw3 salmonella  
42 21 100.0 151 1 TPCS\_BALNU P21798 balanus nub  
43 21 100.0 151 1 YD97\_THETN Q8ra33 thermoaer  
44 21 100.0 151 1 YKA2\_YEAST P36108 saccharomyc  
45 21 100.0 152 1 Y534\_BRUME Q8y1b0 brucella me

#### ALIGNMENTS

##### RESULT 1

FIBB\_SHEEP  
ID FIBB\_SHEEP STANDARD; PRT; 20 AA.  
AC P14470;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).  
GN FGB.  
OS Ovis aries (Sheep), and  
OS Capra hircus (Goat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940, 9925;  
RN [1]  
RP SEQUENCE.  
RA Blomback B., Blomback M., Grondahl N.J.;  
RT "Studies on fibrinopeptides from mammals.";  
RL Acta Chem. Scand. 13:1789-1791(1965).  
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that  
polymerize into fibrin and acting as a cofactor in platelet  
aggregation.  
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
(ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,  
which cleaves fibrinopeptides A and B from alpha and beta chains,  
and thus exposes the N-terminal polymerization sites responsible  
for the formation of the soft clot.  
DR InterPro: IPR002181; Fibrinogen C.  
DR PROSITE: PS00514; FIBRIN AG C DOMAIN; PARTIAL.  
KW Blood coagulation; Plasma; Sulfation.  
FT PEPTIDE 1 20 FIBRINOPEPTIDE B.  
FT MOD\_RES 5 20 SULFATION.  
FT NON\_TER 20 20  
SQ SEQUENCE 20 AA; 2338 MW; PCFSB6FF0DEC6627 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 44;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4

DB 6 DEVD 9

##### RESULT 2

FIBB\_ODOHE  
ID FIBB\_ODOHE STANDARD; PRT; 21 AA.  
AC P14476;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).

GN FGB.

OS Odocoileus hemionus (Mule deer) (Black-tailed deer).

CC Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;  
CC Cervidae; Odocoileinae; Odocoileus.  
OX NCBI\_TaxID=9872;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=67209145; PubMed=6033721;  
RA Doolittle R.F., Schubert D., Schwartz S.A.; fibrinopeptides. I.  
RT "Amino acid sequence studies on artiodactyl fibrinopeptides. I.  
RT Dromedary camel, mule deer, and cape buffalo.";  
RL Arch. Biochem. Biophys. 118:456-467(1967).  
CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that  
CC polymerize into fibrin and acting as a cofactor in platelet  
CC aggregation.  
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,  
CC which cleaves fibrinopeptides A and B from alpha and beta chains,  
CC and thus exposes the N-terminal polymerization sites responsible  
CC for the formation of the soft clot.  
DR InterPro: IPR002181; Fibrinogen C.  
DR PROSITE; PS00514; FIBRIN\_AG\_C DOMAIN; PARTIAL.  
KW Blood coagulation; Plasma; Sulfation; Pyrrolidone carboxylic acid.  
FT PEPTIDE 1 21 FIBRINOPEPTIDE B.  
FT MOD RES 1 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT NON\_TER 21 21 SULFATION.  
SQ SEQUENCE 21 AA; 2496 MW; FCF562C51A0C1627 CRC64;  
Query Match 100.0%; Score 21; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DEVD 4  
DB 7 DEVD 10  
RESULT 3  
YC60 BRAJA STANDARD; PRT; 60 AA.  
AC Q89U29;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Hypothetical zinc-binding UPF0243 protein bsrl260.  
GN BSrl260.  
OS Bradyrhizobium japonicum.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Bradyrhizobiaceae; Bradyrhizobium.  
OX NCBI\_TaxID=375;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=USDA 110;  
RA Kaneo T., Nakamura Y., Sato S., Minamisawa K., Uchiyumi T.,  
RA Sasamoto S., Watanabe A., Igesawa K., Iriyuchi M., Kawashima K.,  
RA Kohara M., Matsumoto M., Shimo S., Tsuruoka H., Wada T., Yamada M.,  
RA Tabata S.;  
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium  
RT Bradyrhizobium japonicum USDA110.";  
RL DNA Res. 9:189-197(2002).  
CC -1- COFACTOR: Binds 1 zinc ion (By similarity).  
CC -1- SIMILARITY: Belongs to the UPF0243 family.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----

DR EMBL; AP005939; BAC46525.1; -.  
DR HAMAP; MF\_00649; -.  
DR InterPro; IPR005584; DUF329.  
DR Pfam; PF03884; DUF329; 1.  
KW Hypothetical protein; zinc; Metal-binding; Complete proteome.  
FT METAL 15 15 ZINC (BY SIMILARITY).  
FT METAL 18 18 ZINC (BY SIMILARITY).  
FT METAL 30 30 ZINC (BY SIMILARITY).  
FT METAL 34 34 ZINC (BY SIMILARITY).  
SQ SEQUENCE 60 AA; 6692 MW; C7DSFFFE0278B1D9 CRC64;  
Query Match 100.0%; Score 21; DB 1; Length 60;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DEVD 4  
DB 54 DEVD 57  
RESULT 4  
MIP BOTAS STANDARD; PRT; 63 AA.  
AC P81077;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Myotoxin inhibitor protein MIP.  
OS Bothrops asper (Terciopelo).  
OC Lepidosauria; Squamata; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Viperidae; Crotalinae; Bothrops.  
OX NCBI\_TaxID=8722;  
RN [1]  
RP SEQUENCE.  
RX TISSUE=Blood;  
RX MEDLINE=97439729; PubMed=9307037;  
RA Lizano S., Lomonte B., Fox J.W., Gutierrez J.M.;  
RT "Biochemical characterization and pharmacological properties of a  
RT phospholipase A2 myotoxin inhibitor from the plasma of the snake  
RT Bothrops asper.";  
RL Biochem. J. 326:853-859(1997).  
CC -1- FUNCTION: Binds to and neutralizes the activities of basic  
CC phospholipase A2 (PLA2) myotoxin isoforms.  
CC -1- SUBUNIT: Oligomer composed of five 23-25 kDa subunits.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.  
KW Glycoprotein; Plasma; Lectin.  
SQ SEQUENCE 63 AA; 7154 MW; F1E6AF75D8489CE6 CRC64;  
Query Match 100.0%; Score 21; DB 1; Length 63;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DEVD 4  
DB 1 DEVD 4  
RESULT 5  
Y858 HELPJ STANDARD; PRT; 67 AA.  
AC Q9ZK37;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Probable tautomerase JHP0858 (EC 5.3.2.-).  
GN JHP0858.  
OS Helicobacter pylori J99 (Campylobacter pylori J99).  
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
OC Helicobacteraceae; Helicobacter.  
OX NCBI\_TaxID=85963;  
RN [1]



RP SEQUENCE FROM N.A.  
RX MEDLINE=99120557; PubMed=9923682;  
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown B.D., Doig P.C.,  
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,  
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,  
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,  
RA Trust T.J.;  
RT "Genomic sequence comparison of two unrelated isolates of the human  
RT gastric pathogen *Helicobacter pylori*.";  
RL Nature 397:176-180(1999).  
CC -!- SIMILARITY: Belongs to the tautomerase family.  
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; AE001515; AAD06434.1; -;  
CC PIR; B71880; B71880.  
CC HAMAP; MF 00718; -; 1.  
CC InterPro: IPR004370; Taut.  
CC Pfam; PF01361; Tautomerase; 1.  
CC ProDom; PD404143; Taut; 1.  
CC TIGRFAMs; TIGR00013; Taut; 1.  
CC Isomerase; Complete proteome.  
KW INIT MET 0  
FT ACT SITE 1 1 CATALYTIC BASE (BY SIMILARITY).  
FT ACT SITE 1 1 CATALYTIC BASE (BY SIMILARITY).  
SQ SEQUENCE 67 AA; 7394 MW; F5AD98AA31A738FB CRC64;  
Query Match 100.0%; Score 21; DB 1; Length 67;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DEVD 4  
DB 46 DEVD 49  
RESULT 6  
Y924\_HELPY  
ID Y924\_HELPY STANDARD; PRT; 67 AA.  
AC Q25581;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Probable tautomerase HP0924 (EC 5.3.2.-).  
GN HP0924.  
OS *Helicobacter pylori* (Campylobacter pylori).  
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
OC Helicobacteraceae; Helicobacter.  
OX NCBI\_TaxID=210;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=26695 / ATCC 700992;  
RX MEDLINE=9739467; PubMed=9252185;  
RA Tomb J.-F., White O., Kervat K.A., Klenk H.-P., Gill S., Dougherty B.A.,  
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Kirschner E.F., Peterson S.,  
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Glodek A.,  
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,  
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,  
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,  
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Matthey L., Wallin E.,  
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,  
RA Venter J.C.;  
RT "The complete genome sequence of the gastric pathogen *Helicobacter*  
RT *pylori*.";  
RL Nature 388:539-547(1997).  
CC -!- SIMILARITY: Belongs to the tautomerase family.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; AE000602; AAD07977.1; -;  
CC PIR; D64635; D64635.  
CC TIGR; HP0924; -;  
CC HAMAP; MF 00718; -; 1.  
CC InterPro: IPR004370; Taut.  
CC Pfam; PF01361; Tautomerase; 1.  
CC ProDom; PD404143; Taut; 1.  
CC TIGRFAMs; TIGR00013; Taut; 1.  
CC Isomerase; Complete proteome.  
KW INIT MET 0  
FT ACT SITE 1 1 CATALYTIC BASE (BY SIMILARITY).  
FT ACT SITE 1 1 CATALYTIC BASE (BY SIMILARITY).  
SQ SEQUENCE 67 AA; 7380 MW; 36AD98AA31A73EE9 CRC64;  
Query Match 100.0%; Score 21; DB 1; Length 67;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DEVD 4  
DB 46 DEVD 49  
RESULT 7  
YE97\_HAEIN  
ID YE97\_HAEIN STANDARD; PRT; 75 AA.  
AC P44221;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Hypothetical protein H1497.  
GN H1497.  
OS *Haemophilus influenzae*.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
OC Pasteurellaceae; *Haemophilus*.  
OX NCBI\_TaxID=727;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Rd / KW20 / ATCC 51907;  
RX MEDLINE=95350630; PubMed=7542800;  
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,  
RA Kervat K.A., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,  
RA McKenney K., Sutton R., Fitch J., Fitch J., Gocayne J.D.,  
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,  
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,  
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,  
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,  
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
RA Venter J.C.;  
RT "Whole-genome random sequencing and assembly of *Haemophilus influenzae*  
RT Rd.";  
RL Science 269:496-512(1995).  
CC -!- SIMILARITY: Contains 1 dksA/trar-type zinc finger.  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
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CC  
CC EMBL; U32826; AAC23137.1; -;  
CC PIR; F64032; F64032.  
CC TIGR; H1497; -;  
CC InterPro: IPR000962; Znf\_dksA\_Trar.  
CC Pfam; PF01258; zf\_dksA\_trar; 1.

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DR PRINTS; PR00618; DKSZNFINGER.
DR PROSITE; PS01102; DKSATRAR_ZN_FINGER; 1.
KW Hypothetical protein; Zinc-finger; Complete proteome.
SQ ZN FING 43 67 TSAR/DKSA-TYPE.
SQ SEQUENCE 75 AA; 8405 MW; 9F6DAD6F2C02C626 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 75;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
Db 31 DEVD 34

RESULT 8
YJDI_ECOLI
ID YJDI_ECOLI STANDARD; PRT; 76 AA.
AC P39273;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein yjdi.
GN YJDI OR B4146 OR B5728 OR ECS5108.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MGL655;
RX MEDLINE=95334362; PubMed=7610040;
RA Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
RA Blattner F.R.;
RT "Analysis of the Escherichia coli genome VI: DNA sequence of the
RL region from 92.8 through 100 minutes.";
RL Nucleic Acids Res. 23:2105-2119(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.F., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RMD 0509952;
RX MEDLINE=21156231; PubMed=1158796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RL O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
CC -----
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CC -----
DR EMBL; U14003; AAA97026.1; -.
DR EMBL; AE000485; AAC7087.1; -.
DR EMBL; AE005646; AAG59325.1; -.

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DR EMBL; AP002568; BAB38531.1; -.
DR FIR; A86108; A86108.
DR FIR; D91267; D91267.
DR FIR; S56355; S56355.
DR EcoGene; EG12466; yjdi.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 76 AA; 8550 MW; 062C085C008C20AC CRC64;

Query Match 100.0%; Score 21; DB 1; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
Db 52 DEVD 55

RESULT 9
MP5A_AMBPS
ID MP5A_AMBPS STANDARD; PRT; 77 AA.
AC P43174;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Pollen allergen Amb p 5a precursor (Amb p Va).
OS Ambrosia psilostachya (Western ragweed).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Campanulids; Asterales; Asteraceae; Asteroidae; Helianthaceae;
OC Ambrosia.
OX NCBI_TaxID=29715;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 23-63.
RC TISSUE=Pollen;
RX MEDLINE=94194048; PubMed=7511632;
RA Ghosh B., Rafnar T., Perry M.P., Bassolino-Klimas D.,
RA Mettler W.J., Klapper D.G., Marsh D.G.;
RT "Immunologic and molecular characterization of Amb p V allergens from
RL Ambrosia psilostachya (western ragweed) pollen.";
RL J. Immunol. 152:2882-2889(1994).
CC -!- ALLERGEN: Causes an allergic reaction in human.
CC -----
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CC -----
DR EMBL; L24465; AAA20065.1; -.
DR EMBL; L24466; AAA20067.1; -.
DR HSSP; P10444; LBGG.
DR InterPro; IPR005611; Amb_V_allergen.
DR Pfam; PF03913; Amb_V_allergen; 1.
DR ProDom; PD018950; Amb_V_allergen; 1.
DR Allergen; Signal.
FT SIGNAL 1 22 POLLEN ALLERGEN AMB P 5A.
FT CHAIN 23 77 BY SIMILARITY.
FT DISULFID 26 61 BY SIMILARITY.
FT DISULFID 33 48 BY SIMILARITY.
FT DISULFID 40 54 BY SIMILARITY.
FT DISULFID 41 65 BY SIMILARITY.
FT VARIANT 59 59 E -> K (IN CLONE A3).
SQ SEQUENCE 77 AA; 8710 MW; 2D8976BE65D9A00F CRC64;

Query Match 100.0%; Score 21; DB 1; Length 77;
Best Local Similarity 100.0%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
Db 15 DEVD 19

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RX MEDLINE=99452783; PubMed=10523320;  
 RA Acheel T., Brahms H., Kastner B., Bachi A., Wilm M., Luehrmann R.;  
 RT "A doughnut-shaped heteromer of human Sm-like proteins binds to the  
 RT 3'-end of U6 snRNA, thereby facilitating U4/U6 duplex formation in  
 RT vitro.";  
 RL EMBO J. 18:5789-5802(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Olavesen M.G., Campbell R.D.;  
 RT "Characterisation of the novel gene G7b located in the class III  
 RT region of the human major histocompatibility complex.";  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A.,  
 RA Abbasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,  
 RA Lasky S., Hood L.;  
 RT "Sequence of the human major histocompatibility complex class III  
 RT region."; (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Shiina S., Tamiya G., Oka A., Inoko H.;  
 RT "Homo sapiens 21229, 817bp genomic DNA of 6p21.3 HLA class I region.";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE=Hypothalamus;  
 RX MEDLINE=20402571; PubMed=10931946;  
 RA Hu R.-M., Han Z.-G., Song H.-D., Peng Y.-D., Huang Q.-H., Ren S.-X.,  
 RA Gu Y.-J., Huang C.-H., Li Y.-B., Jiang C.-L., Fu G., Zhang Q.-H.,  
 RA Gu B.-W., Dai M., Mao Y.-F., Gao G.-F., Rong R., Ye M., Zhou J.,  
 RA Xu S.-H., Gu J., Shi J.-X., Jin W.-R., Zhang C.-K., Wu T.-M.,  
 RA Huang G.-Y., Chen Z., Chen M.-D., Chen J.-L.;  
 RT "Gene expression profiling in the human hypothalamus-pituitary-adrenal  
 RT axis and full-length cDNA cloning.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:9543-9548 (2000).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA Schmarda A., Presser F., Paulmichl M.;  
 RT "Human SMX5 homolog.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE=Placenta;  
 RX MEDLINE=23288257; PubMed=12477932;  
 RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Gasavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: Binds specifically to the 3'-terminal U-tract of U6  
 CC snRNA.  
 CC -1- SUBUNIT: Lsm subunits form a heteromer with a doughnut shape.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).  
 CC -1- SIMILARITY: Belongs to the snRNP Sm proteins family.  
 CC -----  
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RX MEDLINE=99452783; PubMed=10523320;  
 RA Acheel T., Brahms H., Kastner B., Bachi A., Wilm M., Luehrmann R.;  
 RT "A doughnut-shaped heteromer of human Sm-like proteins binds to the  
 RT 3'-end of U6 snRNA, thereby facilitating U4/U6 duplex formation in  
 RT vitro.";  
 RL EMBO J. 18:5789-5802(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Olavesen M.G., Campbell R.D.;  
 RT "Characterisation of the novel gene G7b located in the class III  
 RT region of the human major histocompatibility complex.";  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A.,  
 RA Abbasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,  
 RA Lasky S., Hood L.;  
 RT "Sequence of the human major histocompatibility complex class III  
 RT region."; (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Shiina S., Tamiya G., Oka A., Inoko H.;  
 RT "Homo sapiens 21229, 817bp genomic DNA of 6p21.3 HLA class I region.";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE=Hypothalamus;  
 RX MEDLINE=20402571; PubMed=10931946;  
 RA Hu R.-M., Han Z.-G., Song H.-D., Peng Y.-D., Huang Q.-H., Ren S.-X.,  
 RA Gu Y.-J., Huang C.-H., Li Y.-B., Jiang C.-L., Fu G., Zhang Q.-H.,  
 RA Gu B.-W., Dai M., Mao Y.-F., Gao G.-F., Rong R., Ye M., Zhou J.,  
 RA Xu S.-H., Gu J., Shi J.-X., Jin W.-R., Zhang C.-K., Wu T.-M.,  
 RA Huang G.-Y., Chen Z., Chen M.-D., Chen J.-L.;  
 RT "Gene expression profiling in the human hypothalamus-pituitary-adrenal  
 RT axis and full-length cDNA cloning.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:9543-9548 (2000).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
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 RT "Human SMX5 homolog.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE=Placenta;  
 RX MEDLINE=23288257; PubMed=12477932;  
 RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Gasavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: Binds specifically to the 3'-terminal U-tract of U6  
 CC snRNA.  
 CC -1- SUBUNIT: Lsm subunits form a heteromer with a doughnut shape.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).  
 CC -1- SIMILARITY: Belongs to the snRNP Sm proteins family.  
 CC -----  
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RESULT 10  
 EF1B\_THEAC STANDARD; PRT; 88 AA.  
 AC Q9HKN1;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Elongation factor 1-beta (EF1-beta).  
 GN EF1B OR TA0566.  
 OS Thermoplasma acidophilum.  
 OC Archaea; Euryarchaeota; Thermoplasmatia; Thermoplasmatiales;  
 OC Thermoplasmataceae; Thermoplasma.  
 OX NCBI\_TaxID=2303;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DSM 1728;  
 RX MEDLINE=20479972; PubMed=11029001;  
 RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,  
 RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;  
 RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma  
 RT acidophilum.";  
 RL Nature 407:508-513(2000).  
 CC -1- FUNCTION: Promotes the exchange of GDP for GTP in EF-1-alpha/GDP,  
 CC thus allowing the regeneration of EF-1-alpha/GTP that could then  
 CC be used to form the ternary complex EF-1-alpha/GTP/AATRNA (By  
 CC similarity).  
 CC -1- SIMILARITY: Belongs to the EF-1-beta/EF-1-delta family.  
 CC -----  
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 CC -----  
 DR EMBL; AL445064; CAC11706.1; ALT\_INIT.  
 DR HSP; 027734; IGH8.  
 DR HAMAP; MF\_00043; -; 1.  
 DR InterPro; IPR004542; aEF-1\_beta.  
 DR InterPro; IPR001326; EF1\_BD.  
 DR Pfam; PF00736; EF1BD; 1\_  
 DR TIGRfam; TIGR00489; aEF1\_beta; 1.  
 KW Elongation factor; Protein biosynthesis; Complete proteome.  
 SQ SEQUENCE 88 AA; 9749 MW; 572357C1BADE5DA7 CRC64;  
 Query Match 100.0%; Score 21; DB 1; Length 88;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DEVD 4  
 DB 40 DEVD 43  
 |||||  
 RESULT 11  
 LSM2\_HUMAN STANDARD; PRT; 95 AA.  
 AC Q9Y333;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE U6 snRNA-associated Sm-like protein LSM2 (Small nuclear ribonuclear  
 DE protein D homolog) (G7b) (SnRNP core SM-like protein SM-x5).  
 GN LSM2 OR C6ORF28 OR G7B.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

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CC -----

DR EMBL; AF182288; AAD56226.1; -  
DR EMBL; AJ245416; CAB52190.1; -  
DR EMBL; AF134726; AAD21818.1; -  
DR EMBL; AF000503; BAB63302.1; -  
DR EMBL; AF136977; AAG49438.1; -  
DR EMBL; AF196468; AAG33023.1; -  
DR EMBL; BC009192; AAH09192.1; -  
DR Genew; HGNC:13940; LSM2.  
DR GK; Q9V333; -  
DR MIM; 607282; -  
DR GO; GO:0005634; C:nucleus; NAS.  
DR GO; GO:0017070; F:U6 snRNA binding; NAS.  
DR GO; GO:0000398; P:nuclear mRNA splicing, via spliceosome; NAS.  
DR InterPro; IPR006649; snRNP.  
DR InterPro; IPR001163; snRNP\_Sm.  
DR Pfam; PF01423; LSM; 1.  
DR ProDom; PD020287; snRNP; 1.  
DR SMART; SM00651; Sm; 1.  
DR Nuclear protein; Ribonucleoprotein; mRNA splicing; mRNA processing;  
KW RNA-binding.  
SQ SEQUENCE 95 AA; 10834 MW; 623591A09A6ABACE CRC64;

Query Match 100.0%; Score 21; DB 1; Length 95;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DEVD 4  
Db 75 DEVD 78

RESULT 12  
ID VE7\_HPV44 STANDARD; PRT; 97 AA.  
AC Q80314;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE E7 protein.  
GN E7.  
OS Human papillomavirus type 44.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_TaxID=10592;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Delius H.;  
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: E7 PROTEIN HAS BOTH TRANSFORMING AND TRANS-ACTIVATING  
CC ACTIVITIES.  
CC -----

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CC -----

DR EMBL; U31788; AAA79458.1; -  
DR InterPro; IPR000148; Papvi\_E7.  
DR Pfam; PF00527; E7; 1.  
KW Early protein; Transcription regulation; Oncogene;  
KW DNA-binding; Trans-acting factor.  
FT SITE 57 60 C-XX-C MOTIF-1.  
FT SITE 90 93 C-XX-C MOTIF-2.

SQ SEQUENCE 97 AA; 10641 MW; E4866AE13E050456 CRC64;  
Query Match 100.0%; Score 21; DB 1; Length 97;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DEVD 4  
Db 34 DEVD 37

RESULT 13  
ID VE7\_HPV55 STANDARD; PRT; 97 AA.  
AC Q80935;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE E7 protein.  
GN E7.  
OS Human papillomavirus type 55.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_TaxID=37114;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Delius H.;  
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: E7 PROTEIN HAS BOTH TRANSFORMING AND TRANS-ACTIVATING  
CC ACTIVITIES.  
CC -----

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CC -----

DR EMBL; U31791; AAA79479.1; -  
DR InterPro; IPR000148; Papvi\_E7.  
DR Pfam; PF00527; E7; 1.  
KW Early protein; Transcription regulation; Oncogene;  
KW DNA-binding; Trans-acting factor.  
FT SITE 57 60 C-XX-C MOTIF-1.  
FT SITE 90 93 C-XX-C MOTIF-2.  
SQ SEQUENCE 97 AA; 10621 MW; E2997616BCE47D42 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 97;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DEVD 4  
Db 34 DEVD 37

RESULT 14  
ID YG79\_METJA STANDARD; PRT; 97 AA.  
AC Q59073;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein MJ1679.  
GN MJ1679.  
OS Methanococcus jannaschii.  
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;  
OC Methanocaldococaceae; Methanocaldococcus.  
OX NCBI\_TaxID=2190;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

```

RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervatage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RL Science 273:1058-1073(1996).
CC -----
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CC -----
CC EMBL; U67607; AAB99704.1; -.
DR EMBL; U67607; AAB99704.1; -.
DR PIR; E64509; E64509.
DR TIGR; M01679; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 97 AA; 11880 MW; 64C59303B9101FE0 CRC64;
Query Match 100.0%; Score 21; DB 1; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DEVD 4
DB 82 DEVD 85
RESULT 15
VE7 HPV11 STANDARD; PRT; 98 AA.
ID VE7 HPV11
AC P04020;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE E7 protein.
GN E7.
OS Human papillomavirus type 11.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
CC Papillomavirus.
CC NCBI_TaxID=10580;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86181601; PubMed=3008427;
RA Dartmann K., Schwarz E., Giesmann L., Zur Hausen H.;
RT "The nucleotide sequence and genome organization of human papilloma
RT virus type 11."
RL Virology 151:124-130(1986).
RN [2]
RP SEQUENCE FROM N.A.
RA Fife K.H., Fan L., Fritsch M.H., Bryan J., Brown D.R.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: E7 PROTEIN HAS BOTH TRANSFORMING AND TRANS-ACTIVATING
CC ACTIVITIES.
CC -!- SIMILARITY: LOCAL WITH ADENOVIRUS EA AND SV40 LT.
CC -----
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CC -----
CC EMBL; M14119; AAA46928.1; -.

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DR EMBL; L36108; AAA21704.1; -.
DR PIR; A03690; W7KL11.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
KW Early protein; Transcription regulation; Oncogene;
KW DNA-binding; Trans-acting factor.
FT SITE 58 61 C-XX-C MOTIF-1.
FT SITE 91 94 C-XX-C MOTIF-2.
SQ SEQUENCE 98 AA; 10889 MW; AACAA9A60C933E1F6 CRC64;
Query Match 100.0%; Score 21; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DEVD 4
DB 35 DEVD 38
Search completed: May 24, 2004, 14:39:34
Job time : 11.5 secs

```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 24, 2004, 14:36:17 ; Search time 36.5 Seconds  
(without alignments)  
34.577 Million cell updates/sec

Title: US-09-765-105A-2

Perfect score: 21

Sequence: 1 DEVD 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL\_25.\*

1: sp\_archaea.\*

2: sp\_bacteria.\*

3: sp\_fungi.\*

4: sp\_human.\*

5: sp\_invertebrate.\*

6: sp\_mammal.\*

7: sp\_mhc.\*

8: sp\_organelle.\*

9: sp\_phage.\*

10: sp\_plant.\*

11: sp\_rodent.\*

12: sp\_virus.\*

13: sp\_vertebrate.\*

14: sp\_unclassified.\*

15: sp\_rvirus.\*

16: sp\_bacteriap.\*

17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	21	100.0	11	10	082070
2	21	100.0	44	2	Q51913
3	21	100.0	45	10	Q49798
4	21	100.0	45	16	Q97087
5	21	100.0	45	16	Q8FVL6
6	21	100.0	49	4	Q8EP95
7	21	100.0	49	5	Q9XVP5
8	21	100.0	50	11	Q63952
9	21	100.0	53	13	Q9IAB6
10	21	100.0	53	16	Q98I88
11	21	100.0	54	9	Q38258
12	21	100.0	54	9	Q38280
13	21	100.0	54	10	Q84NR3
14	21	100.0	54	17	Q977A0
15	21	100.0	56	12	Q99H60
16	21	100.0	56	12	Q99H57

17	21	100.0	56	12	Q99H59	Q99H59 human picob
18	21	100.0	57	10	Q8LH38	Q8LH38 cryza sativ
19	21	100.0	57	16	Q8NPJ7	Q8NPJ7 corynebacte
20	21	100.0	59	5	Q94755	Q94755 schistosoma
21	21	100.0	60	2	Q93AL7	Q93AL7 clostridium
22	21	100.0	60	10	Q7XEA8	Q7XEA8 cryza sativ
23	21	100.0	60	17	Q26625	Q26625 methanobact
24	21	100.0	62	16	Q98IK2	Q98IK2 rhizobium l
25	21	100.0	63	2	Q83XT1	Q83XT1 shigella dy
26	21	100.0	63	17	Q8PTV7	Q8PTV7 methanosarc
27	21	100.0	65	2	Q83XT8	Q83XT8 shigella bo
28	21	100.0	65	13	Q9PTR0	Q9PTR0 brachydanio
29	21	100.0	65	16	Q8FE32	Q8FE32 corynebacte
30	21	100.0	66	10	Q42235	Q42235 arabidopsis
31	21	100.0	66	16	Q83SA5	Q83SA5 enterococcu
32	21	100.0	67	2	Q86180	Q86180 bacteroides
33	21	100.0	67	2	Q83XT3	Q83XT3 shigella bo
34	21	100.0	67	12	Q8VAS6	Q8VAS6 white spot
35	21	100.0	68	16	Q8CMB4	Q8CMB4 vibrio vuln
36	21	100.0	69	2	Q83XT7	Q83XT7 shigella so
37	21	100.0	69	2	Q83XS7	Q83XS7 shigella dy
38	21	100.0	69	16	Q9JRE9	Q9JRE9 neisseria m
39	21	100.0	70	12	Q8VES0	Q8VES0 halovirus h
40	21	100.0	70	12	Q7TDK9	Q7TDK9 halovirus h
41	21	100.0	70	16	Q9CJQ9	Q9CJQ9 pasteurella
42	21	100.0	71	2	Q83XU0	Q83XU0 shigella dy
43	21	100.0	71	2	Q83XT6	Q83XT6 shigella bo
44	21	100.0	71	2	Q83XT2	Q83XT2 shigella fl
45	21	100.0	71	2	Q83XS8	Q83XS8 shigella dy

#### ALIGNMENTS

#### RESULT 1

082070 PRELIMINARY; PRT; 11 AA.  
ID 082070  
AC 082070;  
DT 01-NOV-1998 (TRENBLrel. 08, Created)  
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE RNA polymerase (EC 2.7.7.6) (Fragment).  
OS Triticum aestivum (wheat).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Triticum.  
OX NCBI\_TaxID=4565;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=cnv. Chinese Spring;  
RA Young D.A.; Allen R.; Harvey A.J.; Lonsdale D.M.;  
RT "Characterization of a gene encoding a single-subunit RNA polymerase  
from maize which is alternatively spliced."  
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ005344; CAA06489.1;  
DR GO; GO:0003899; F:DNA-directed RNA polymerase activity; IEA.  
DR GO; GO:0003900; F:DNA-directed RNA polymerase I activity; IEA.  
DR GO; GO:0003901; F:DNA-directed RNA polymerase II activity; IEA.  
DR GO; GO:0003902; F:DNA-directed RNA polymerase III activity; IEA.  
KW Nucleotidyltransferase; Transferase.  
FT NON\_TER 1  
FT NON\_TER 11  
SQ SEQUENCE 11 AA; 1329 MW; CD96344923240AB2 CRC64;

Query Match 100.0%; Score 21; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4

Db 2 DEVD 5

```

Db      19 DEVD 22

RESULT 2
Q51913  PRELIMINARY;      PRT;      44 AA.
AC Q51913;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DE HMG-CoA-reductase (Fragment).
OS Pseudomonas mevalonii.
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=32044;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90078086; PubMed=2687235;
RA Anderson D.H., Rodwell V.W.;
RT "Nucleotide sequence and expression in Escherichia coli of the 3-
RT hydroxy-3-methylglutaryl coenzyme A lyase gene of Pseudomonas
RT mevalonii."
RL J. Bacteriol. 171:6469-6472(1989).
DR EMBL; M31807; AAA25894.1; -.
DR GO; GO:0004420; P:hydroxymethylglutaryl-CoA reductase (NADPH). . .; IEA.
DR GO; GO:0009058; P:biogenesis; IEA.
DR InterPro; IPR002202; HMG-CoA_red.
DR InterPro; IPR009029; HMG-CoA_sub_bind.
DR Pfam; PF00368; HMG-CoA_red; 1.
FT NON_TER 1
SQ SEQUENCE 44 AA; 4925 MW; 9722E2A58DEB5193 CRC64;

Query Match 100.0%; Score 21; DB 2; Length 44;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
DB 14 DEVD 17

RESULT 3
O49798  PRELIMINARY;      PRT;      45 AA.
AC O49798;
DT 01-JUN-1998 (T-EMBLrel. 06, Created)
DT 01-JUN-1998 (T-EMBLrel. 06, Last sequence update)
DE R2R3-MYB transcription factor (Fragment).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eustoids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX Romero I., Fuentes A., Benito M.J., Malpica J., Leyva A., Paz-Ares J.;
RT "One hundred R2R3-MYB genes in the genome of Arabidopsis thaliana.";
RT Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z95798; CAB09230.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001005; MYB_DNA_binding.
DR Pfam; PF00249; myb_DNA-binding; 1.
DR PROSITE; PS50090; MYB_3; 1.
FT NON_TER 1
FT NON_TER 45
SQ SEQUENCE 45 AA; 5308 MW; A5A8E1509F3D6376 CRC64;

Query Match 100.0%; Score 21; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
DB 14 DEVD 17

```

```

Db      19 DEVD 22

RESULT 4
Q97087  PRELIMINARY;      PRT;      45 AA.
AC Q97087;
DT 01-OCT-2001 (T-EMBLrel. 18, Created)
DT 01-OCT-2001 (T-EMBLrel. 18, Last sequence update)
DE 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Hypothetical protein SPI339.
GN SPI339.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC BAA-334 / TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae."
RL Science 293:498-506(2001).
DR EMBL; AE007432; AAK75437.1; -.
DR PIR; D95155; D95155.
DR TIGR; SPI339; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 45 AA; 5089 MW; FOA7B635C2683F20 CRC64;

Query Match 100.0%; Score 21; DB 16; Length 45;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
DB 19 DEVD 22

RESULT 5
Q8FVL6  PRELIMINARY;      PRT;      45 AA.
AC Q8FVL6;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DE Hypothetical protein.
GN BRA0821.
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=1330 / Biovar 1;
RX MEDLINE=22247741; PubMed=12271122;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
RA Dougherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,
RA Redmiller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
RT animal and plant pathogens and symbionts."
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
DR EMBL; AE014576; AAN39996.1; -.

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DR TIGR; BRA0821; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 45 AA; 5041 MW; 7F27B6874E77F886 CRC64;

Query Match      100.0%; Score 21; DB 16; Length 45;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
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Db 3 DEVD 6

RESULT 6
Q96P95 PRELIMINARY; PRT; 49 AA.
ID Q96P95
AC Q96P95;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Poly(ADP-ribose) polymerase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Kang H.S., Park Y.-J., Jung H.M., Jun D.Y., Huh T.L., Kim Y.H.;
RT "Characterization of TPA-responsive genes in U937 cells using ordered
RT differential display PCR.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF401218; AL02174.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001510; Znf_PolyADPpol.
DR Pfam; PF00645; zf-PARP; 1.
DR ProDom; PD004675; Znf_PolyADPpol; 1.
DR PROSITE; PS00064; PARP_ZN_FINGER_2; 1.
FT NON_TER 1
FT NON_TER 49
FT NON_TER 49
SQ SEQUENCE 49 AA; 5300 MW; 68F91BA7DABDF4A5 CRC64;

Query Match      100.0%; Score 21; DB 4; Length 49;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
   ||||
Db 34 DEVD 37

RESULT 7
Q9XVP5 PRELIMINARY; PRT; 49 AA.
ID Q9XVP5
AC Q9XVP5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE F35C12.1 protein.
DE F35C12.1 protein.
GN F35C12.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoides;
OC Rhabditidae; Pterodermidae; Caenorhabditis.
OC NCBI_TaxID=6239;
RN [1]
SEQUENCE FROM N.A.
RA Baynes C.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RA "Genome sequence of the nematode C.elegans: A platform for
RT

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RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z81075; CAB03046.1; -.
DR PIR; T21746; T21746.
DR WormPep; F35C12.1; CE09913.
SQ SEQUENCE 49 AA; 5597 MW; 778CB60EB83DPEBE CRC64;

Query Match      100.0%; Score 21; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
   ||||
Db 33 DEVD 36

RESULT 8
Q63952 PRELIMINARY; PRT; 50 AA.
ID Q63952
AC Q63952;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Endoplasmin (Fragment).
DE GRP94.
GN GRP94.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OC NCBI_TaxID=10118;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=94148528; PubMed=8314313;
RA De Vouge M.W., Yamazaki A., Bennett S.A., Chen J.H., Shwed P.S.,
RA Couture C., Birnboim H.C.;
RT "Immunoselection of GRP94/endoplasmin from a KNRK cell-specific lambda
RT still library using antibodies directed against a putative heparanase
RT amino-terminal peptide.";
RL Int. J. Cancer 56:286-294(1994).
DR EMBL; S69315; AA829919.2; -.
FT NON_TER 50
FT NON_TER 50
SQ SEQUENCE 50 AA; 5478 MW; D8866A965A646117 CRC64;

Query Match      100.0%; Score 21; DB 11; Length 50;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4
   ||||
Db 23 DEVD 26

RESULT 9
Q9IAB6 PRELIMINARY; PRT; 53 AA.
ID Q9IAB6
AC Q9IAB6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SMX5 (Fragment).
DE SMX5.
GN SMX5.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
SEQUENCE FROM N.A.
RA Suellmann H., Murray B.W., Klein J.;
RT "Analysis of Ancient Mhc Class III Synteny by Mapping of Orthologous
RT Genes in the Zebrafish.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF210645; AAF70450.1; -.
DR ZFIN; ZDB-GENE-000616-10; smx5.

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DR GO: 0005634; C:nucleus; IEA.  
DR GO: 0005732; C:small nucleolar ribonucleoprotein complex; IEA.  
DR GO: 0008248; F:pre-mRNA splicing factor activity; IEA.  
DR GO: 0006371; F:mRNA splicing; IEA.  
DR InterPro: IPR006649; snRNP.  
DR InterPro: IPR001163; snRNP\_Sm.  
DR Pfam: PF01423; LSM; 1.  
DR ProDom: PD020287; snRNP; 1.  
FT NON\_TER 1 1  
FT NON\_TER 53 53  
SQ SEQUENCE 53 AA; 6078 MW; E70502074A527393 CRC64;

Query Match 100.0%; Score 21; DB 13; Length 53;  
Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4  
Db 48 DEVD 51

RESULT 10  
Q98IM8 PRELIMINARY; PRT; 53 AA.  
AC Q98IM8; 01-OCT-2001 (TrEMBLrel. 18, Created)  
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Hypothetical protein mar2334.  
GN MSR2334.  
OS Rhizobium loti (Mesorhizobium loti).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Phyllobacteriaceae; Mesorhizobium.  
OX NCBI\_TaxID=381;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MAFF303099;  
EX MEDLINE=21082930; PubMed=11214968;  
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
RA Watanabe A., Ideawa K., Ishikawa A., Kawashima K., Kimura T.,  
RA Kishida Y., Kiyokawa C., Kohara M., Matsunoto M., Matsuno A.,  
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,  
RA Takeuchi C., Yamada M., Tabata S.;  
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
RT Mesorhizobium loti.";  
RL DNA Res. 7:331-338(2000).  
DR EMBL; AP002995; BAB49488.1; -;  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 53 AA; 5289 MW; B7C5B786C6D8279 CRC64;

Query Match 100.0%; Score 21; DB 16; Length 53;  
Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4  
Db 10 DEVD 13

RESULT 11  
Q38258 PRELIMINARY; PRT; 54 AA.  
AC Q38258;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Unidentified ORF15.  
OS Lactococcus phage b1167.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;  
OC C2-like viruses.  
OX NCBI\_TaxID=36343;  
RN [1]  
RP SEQUENCE FROM N.A.

RX MEDLINE=95111629; PubMed=7812447;  
RA Schouler C., Ehrlich S.D., Chopin M.C.;  
RT "Sequence and organization of the lactococcal prolate-headed b1167  
RT phage genome.";  
RL Microbiology 140:3061-3069(1994).  
DR EMBL; L33769; AAA74352.1; -;  
SQ SEQUENCE 54 AA; 6378 MW; F2D42F16S9BF751 CRC64;

Query Match 100.0%; Score 21; DB 9; Length 54;  
Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4  
Db 10 DEVD 13

RESULT 12  
Q38280 PRELIMINARY; PRT; 54 AA.  
AC Q38280; 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE E17 protein.  
GN E17.  
OS Lactococcus bacteriophage c2.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;  
OC C2-like viruses.  
OX NCBI\_TaxID=31537;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94036453; PubMed=8221377;  
RA Ward L.J., Beresford T.P., Lubbers M.W., Jarvis B.D., Jarvis A.W.;  
RT "Sequence analysis of the lysin gene region of the prolate lactococcal  
RT bacteriophage c2.";  
RL Can. J. Microbiol. 39:767-774(1993).  
RN [2]

RP SEQUENCE FROM N.A.  
RX MEDLINE=95115663; PubMed=7816023;  
RA Lubbers M.W., Ward L.J., Beresford T.P., Jarvis B.D., Jarvis A.W.;  
RT "Sequencing and analysis of the cos region of the lactococcal  
RT bacteriophage c2.";  
RL Mol. Gen. Genet. 245:160-166(1994).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96086019; PubMed=8534101;  
RA Lubbers M.W., Waterfield N.R., Beresford T.P., Le Page R.W.,  
RA Jarvis A.W.;  
RT "Sequencing and analysis of the prolate-headed lactococcal  
RT bacteriophage c2 genome and identification of the structural genes.";  
RL Appl. Environ. Microbiol. 61:4348-4356(1995).  
DR EMBL; L48605; AAA92163.1; -;  
SQ SEQUENCE 54 AA; 6453 MW; EA5811217531F751 CRC64;

Query Match 100.0%; Score 21; DB 9; Length 54;  
Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEVD 4  
Db 10 DEVD 13

RESULT 13  
Q84NR3 PRELIMINARY; PRT; 54 AA.  
ID Q84NR3;  
AC Q84NR3;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE P0034A04.6 protein.  
GN P0034A04.6.

OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzoideae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Nipponbare;  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC  
RT clone: P0034A04";  
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AP004333; BAC75552.1; -;  
SQ SEQUENCE 54 AA; 6002 MW; 1B425F6484151E8B CRC64;  
Query Match 100.0%; Score 21; DB 10; Length 54;  
Best Local Similarity 100.0%; Pred. NO. 8.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
Db 35 DEVD 38  
PRT; 54 AA.

RESULT 14  
Q977A0 PRELIMINARY;  
ID Q977A0 PRELIMINARY; PRT; 54 AA.  
AC Q977A0;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Putative alcohol dehydrogenase.  
GN STS015.  
OS Sulfolobus tokodaii.  
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;  
OC Sulfolobus.  
OX NCBI\_TaxID=111955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=JCM 10545 / 7;  
RX MEDLINE=21456156; PubMed=11572479;  
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,  
RA Sekine M., Baba S.-I., Ankaei A., Koeugi H., Hosoyama A., Fukui S.,  
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,  
RA Yoshizawa T., Tanaka T., Kudo Y., Kishida N., Oguchi A.,  
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,  
RA Oshima T., Kikuchi H.;  
RT "Complete genome sequence of an aerobic thermophilic  
RT Crenarchaeon, Sulfolobus tokodaii strain 7."  
RL DNA Res. 8:123-140(2001).  
DR EMBL: AP000981; BAB494.1; -;  
DR GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.  
DR GO; GO:0008270; F:zinc ion binding; IEA.  
DR InterPro; IPR002085; Adh zn family.  
DR Pfam; PF00107; ADH zinc N; 1.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 54 AA; 6138 MW; 132B3C067738F740 CRC64;

Query Match 100.0%; Score 21; DB 17; Length 54;  
Best Local Similarity 100.0%; Pred. NO. 8.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
Db 16 DEVD 19  
PRT; 56 AA.

RESULT 15  
Q99H60 PRELIMINARY;  
ID Q99H60 PRELIMINARY; PRT; 56 AA.  
AC Q99H60;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE RNA-dependent RNA polymerase (Fragment).  
OS Human picobirnavirus  
OC Viruses; dsRNA viruses; Picobirnavirus.  
OX NCBI\_TaxID=145856;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=202-FL-97;  
RX MEDLINE=20534978; PubMed=11080479;  
RA Rosen B.I., Fang Z.Y., Glass R.I., Monroe S.S.;  
RT "Cloning of human picobirnavirus genomic segments and development of  
RT an RT-PCR detection assay";  
RL Virology 277:316-329(2000).  
DR EMBL: AF246935; AAC53579.1; -;  
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.  
KW RNA-directed RNA polymerase.  
FT NON TER 1 56  
FT NON TER 56 56  
SQ SEQUENCE 56 AA; 6708 MW; 781490BF8EB423A9 CRC64;  
Query Match 100.0%; Score 21; DB 12; Length 56;  
Best Local Similarity 100.0%; Pred. NO. 9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEVD 4  
Db 31 DEVD 34  
PRT; 34 AA.

Search completed: May 24, 2004, 14:41:01  
Job time : 37.5 secs